

SEQUENCE LISTING

GENERAL INFORMATION

(i) APPLICANT: Murphy, Patricia

White, Marga Olson, Sheri

Yoshikawa, Matthew Jackson, Geoffrey Eskanderi, Tara Schryer, Brenda Park, Michael

- (ii) TITLE OF THE INVENTION: NOVEL CODING SEQUENCE HAPLOTYPES OF THE HUMAN BRCA2 GENE
- (iii) NUMBER OF SEQUENCES: 133
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Morgan, Lewis & Bockius LLP
 - (B) STREET: 1800 M St., NW
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/084,471
 - (B) FILING DATE: 22 May 1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/055,784
 - (B) FILING DATE: 15 August 1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/064,926
 - (B) FILING DATE: 07 November 1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/065,367
 - (B) FILING DATE: 12 November 1997
- (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 09/071,715
- (B) FILING DATE: 01 May 1998
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Reid G. Adler
 - (B) REGISTRATION NUMBER: 30,988
 - (C) REFERENCE/DOCKET NUMBER: 44921-5058-01-US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-467-7000
 - (B) TELEFAX: 202-467-7258
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 26...75
 - (D) OTHER INFORMATION: Exon 5
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGGGATTTGC TTTGTTTTAT TTTAGTCCTG TTGTTCTACA ATGTACACAT GTAACACCAC 60 AAAGAGATAA GTCAGGTATG ATTAAAAACA ATGCTTTTTA TTCTT 105

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 29...210
 - (D) OTHER INFORMATION: Exon 15¥
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTTTGCTAA GTATTTATTC TTTGATAGAT TTAATTACAA GTCTTCAGAA TGCCAGAGAT 60
ATACAGGATA TGCGAATTAA GAAGAAACAA AGGCAACGCG TCTTTCCACA GCCAGGCAGT 12 0
CAAGTTCCTC CAAAAACATC CACTCTGCCT CGAATCTCTC TGAAAGCAGC AGTAGGAGGC 18 0
CAAGTTCCCT CTGCGTGTTC TCATAAACAG GTATGTGT 21 8

(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 258 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
 (ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE (A) NAME/KEY: exon (B) LOCATION: 34221 (D) OTHER INFORMATION: Exon 16 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
tttttcttt ttgtgtgtgt ttattttgtg tagctgtata cgtatggcgt ttctaaacat tgcataaaaa ttaacagcaa aaatgcagag tcttttcagt ttcacactga agattatttt ggtaaggaaa gtttatggac tggaaaagga atacagttgg ctgatggtgg atggctcata ccctccaatg atggaaaggc tggaaaagaa gaattttata ggtactctat gcaaaaagat tgtgtgttaa cttttatg	120
(2) INFORMATION FOR SEQ ID NO:4:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10485 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA 	
(ix) FEATURE:	
(A) NAME/KEY: Coding Sequence (B) LOCATION: 22910482 (D) OTHER INFORMATION: BRCA2 (OMI1)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCCC TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG ACAGATTTGT GACCGGCGCG GTTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT	120

CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC

Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT

5

237

285

333

Met Pro Ile

1

20					25					30					35	
TC' Se:	T TC	A GA r Gl	A GC: u Ala	F CCA a Pro 40	A CCO	С ТАТ Э Туз	r Aa'	T TC' n Sei	F GAZ Gli 45	A CC' 1 Pro	r gca o Ala	A GAZ a Glu	A GAZ 1 Glu	A TC: 1 Sei 50	ľ GAA r Glu	381
CA' Hi	r aaz s Lys	AAA S Ası	C AA(n Asr 55	C AAT n Asr	Г ТА(1 Туі	C GAZ C Glu	A CC	A AAC Asr 60	C CTA	A TT	r AAA	A ACT	CCA Pro 65	A CAZ o Glr	A AGG n Arg	429
AA? Lys	A CCA S Pro	TC: Sei 70	TAT Tyr	AAT Asn	CAC Glr	G CTC	GC: Ala 75	r TCA a Ser	ACT Thr	CCA Pro	A ATA	A ATA	TTC Phe	C AAA	A GAG s Glu	477
CA7 Glr	A GGG n Gly 85	CTC Let	F ACT	CTG	CCC Pro	CTG Leu 90	TAC	C CAA	TCT Ser	CCT Pro	GTA Val 95	AAA Lys	GAA Glu	TTA Leu	GAT Asp	525
AAA Lys 100	Phe	AAA Lys	TTA Leu	GAC Asp	Leu 105	Gly	AGG Arg	AAT Asn	GTT Val	CCC Pro	Asn	' AGT Ser	'AGA 'Arg	. CAT His	AAA Lys 115	573
AGT Ser	CTT Leu	CGC Arg	ACA Thr	GTG Val 120	Lys	ACT Thr	AAA Lys	ATG Met	GAT Asp 125	CAA Gln	GCA Ala	GAT Asp	GAT Asp	GTT Val 130	TCC Ser	621
TGT Cys	CCA Pro	CTT Leu	CTA Leu 135	AAT Asn	TCT Ser	TGT Cys	CTT Leu	AGT Ser 140	GAA Glu	AGT Ser	CCT Pro	GTT Val	GTT Val 145	CTA Leu	CAA Gln	669
TGT Cys	ACA Thr	CAT His 150	GTA Val	ACA Thr	CCA Pro	CAA Gln	AGA Arg 155	GAT Asp	AAG Lys	TCA Ser	GTG Val	GTA Val 160	TGT Cys	GGG Gly	AGT Ser	717
TTG Leu	TTT Phe 165	CAT His	ACA Thr	CCA Pro	AAG Lys	TTT Phe 170	GTG Val	AAG Lys	GGT Gly	CGT Arg	CAG Gln 175	ACA Thr	CCA Pro	AAA Lys	CAT His	765
ATT Ile 180	TCT Ser	GAA Glu	AGT Ser	CTA Leu	GGA Gly 185	GCT Ala	GAG Glu	GTG Val	GAT Asp	CCT Pro 190	GAT Asp	ATG Met	TCT Ser	TGG Trp	TCA Ser 195	813
AGT Ser	TCT Ser	TTA Leu	GCT Ala	ACA Thr 200	CCA Pro	CCC Pro	ACC Thr	CTT Leu	AGT Ser 205	TCT Ser	ACT Thr	GTG Val	CTC Leu	ATA Ile 210	GTC Val	861
AGA Arg	AAT Asn	GAA Glu	GAA Glu 215	GCA Ala	TCT Ser	GAA Glu	ACT Thr	GTA Val 220	TTT Phe	CCT Pro	CAT His	GAT Asp	ACT Thr 225	ACT Thr	GCT Ala	909
AAT Asn	GTG Val	AAA Lys	AGC Ser	TAT Tyr	TTT Phe	TCC Ser	AAT Asn	CAT His	GAT Asp	GAA Glu	AGT Ser	CTG Leu	AAG Lvs	AAA Lvs	AAT Agn	957

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	GAT Asp	AGA Arg 245	J Ph∈	T ATO	C GC	r TCT a Ser	GTG Val 250	Thi	A GAC	C AG	r gaz c Glu	A AAC 1 Asr 255	Th	A AA'	T CAZ	A AGA n Arg	1005
•	GAA Glu 260	GCT Ala	GCA Ala	AGT Ser	CAT His	GGA Gly 265	Phe	GGA	A AAZ / Lys	A ACI	TCA Ser 270	Gly	AAT Ası	r TC2 n Sen	A TTT	AAA Lys 275	1053
1	GTA Val	AAT Asn	AGC Ser	TGC Cys	Lys 280	Asp	CAC	ATT Ile	GGA Gly	AAG Lys 285	Ser	ATG Met	CCA	A AAT Asr	GTC Val 290	CTA Leu	1101
(GAA Glu	GAT Asp	'GAA Glu	GTA Val 295	Tyr	GAA Glu	ACA Thr	GTT Val	GTA Val	Asp	ACC Thr	TCT Ser	GAA Glu	GAA Glu 305	Asp	'AGT Ser	1149
I	ΓΤΤ ?he	TCA Ser	TTA Leu 310	TGT Cys	TTT Phe	TCT Ser	AAA Lys	TGT Cys 315	Arg	ACA Thr	AAA Lys	. AAT Asn	CTA Leu 320	Gln	AAA Lys	GTA Val	1197
P	AGA Arg	ACT Thr 325	AGC Ser	AAG Lys	ACT Thr	AGG Arg	AAA Lys 330	AAA Lys	ATT	TTC Phe	CAT His	GAA Glu 335	GCA Ala	AAC Asn	GCT Ala	GAT Asp	1245
G	SAA Slu 40	TGT Cys	GAA Glu	AAA Lys	TCT Ser	AAA Lys 345	AAC Asn	CAA Gln	GTG Val	AAA Lys	GAA Glu 350	AAA Lys	TAC Tyr	TCA Ser	TTT Phe	GTA Val 355	1293
I	CT er	GAA Glu	GTG Val	GAA Glu	CCA Pro 360	AAT Asn	GAT Asp	ACT Thr	GAT Asp	CCA Pro 365	TTA Leu	GAT Asp	TCA Ser	AAT Asn	GTA Val 370	GCA Ala	1341
C H	AT	CAG Gln	AAG Lys	CCC Pro 375	TTT Phe	GAG Glu	AGT Ser	GGA Gly	AGT Ser 380	GAC Asp	AAA Lys	ATC Ile	TCC Ser	AAG Lys 385	GAA Glu	GTT Val	1389
G V	TA al	CCG Pro	TCT Ser 390	TTG Leu	GCC Ala	TGT Cys	Glu	${ t Trp}$	Ser	CAA Gln	CTA Leu	ACC Thr	CTT Leu 400	TCA Ser	GGT Gly	CTA Leu	1437
A:	sn (GGA Gly 405	GCC Ala	CAG Gln	ATG Met	GAG Glu	AAA Lys 410	ATA Ile	CCC Pro	CTA Leu	TTG Leu	CAT His 415	ATT Ile	TCT Ser	TCA Ser	TGT Cys	1485
As	AC (sp (20	CAA Gln	AAT Asn	ATT Ile	TCA Ser	GAA Glu 425	AAA Lys	GAC Asp	CTA Leu	TTA Leu	GAC Asp 430	ACA Thr	GAG Glu	AAC Asn	AAA Lys	AGA Arg 435	1533
ΑZ	AG A ys 1	AAA Lys	GAT Asp	TTT Phe	CTT Leu	ACT Thr	TCA Ser	GAG Glu	AAT Asn	TCT Ser	TTG Leu	CCA Pro	CGT Arg	ATT Ile	TCT Ser	AGC Ser	1581

			440					445					450		
CTA CCA Leu Pro	Lys	TCA Ser 455	GAG Glu	AAG Lys	CCA Pro	TTA Leu	AAT Asn 460	GAG Glu	GAA Glu	ACA Thr	GTG Val	GTA Val 465	Asn	AAG Lys	1629
AGA GAT Arg Asp	GAA Glu 470	GAG Glu	CAG Gln	CAT His	CTT Leu	GAA Glu 475	TCT Ser	CAT His	ACA Thr	GAC Asp	TGC Cys 480	ATT	CTT Leu	GCA Ala	1677
GTA AAG Val Lys 485	CAG (GCA Ala	ATA Ile	TCT Ser	GGA Gly 490	ACT Thr	TCT Ser	CCA Pro	GTG Val	GCT Ala 495	TCT Ser	TCA Ser	TTT Phe	CAG Gln	1725
GGT ATC Gly Ile 500	AAA :	AAG Lys	TCT Ser	ATA Ile 505	TTC Phe	AGA Arg	ATA Ile	AGA Arg	GAA Glu 510	TCA Ser	CCT Pro	AAA Lys	GAG Glu	ACT Thr 515	1773
TTC AAT Phe Asn	GCA A	AGT Ser	TTT Phe 520	TCA Ser	GGT Gly	CAT His	ATG Met	ACT Thr 525	GAT Asp	CCA Pro	AAC Asn	TTT Phe	AAA Lys 530	AAA Lys	1821
GAA ACT Glu Thr	Glu A	GCC Ala 535	TCT Ser	GAA Glu	AGT Ser	GGA Gly	CTG Leu 540	GAA Glu	ATA Ile	CAT His	ACT Thr	GTT Val 545	TGC Cys	TCA Ser	1869
CAG AAG Gln Lys	GAG (Glu <i>I</i> 550	GAC Asp	TCC Ser	TTA Leu	TGT Cys	CCA Pro 555	AAT Asn	TTA Leu	ATT Ile	GAT Asp	AAT Asn 560	GGA Gly	AGC Ser	TGG Trp	1917
CCA GCC Pro Ala 565	ACC F	ACC . Thr	ACA Thr	CAG Gln	AAT Asn 570	TCT Ser	GTA Val	GCT Ala	TTG Leu	AAG Lys 575	AAT Asn	GCA Ala	GGT Gly	TTA Leu	1965
ATA TCC . Ile Ser 580	ACT T	TTG . Leu :	Ĺуs	AAG Lys 585	AAA Lys	ACA Thr	AAT Asn	AAG Lys	TTT Phe 590	ATT Ile	TAT Tyr	GCT Ala	ATA Ile	CAT His 595	2013
GAT GAA A	ACA T	er :	FAT Fyr 600	AAA Lys	GGA Gly	AAA Lys	AAA Lys	ATA Ile 605	CCG Pro	AAA Lys	GAC Asp	CAA Gln	AAA Lys 610	TCA Ser	2061
GAA CTA A	Ile A	AC : sn (rgt Cys	TCA Ser	GCC Ala	Gln	TTT Phe 620	GAA Glu	GCA Ala	AAT Asn	Ala	TTT Phe 625	GAA Glu	GCA Ala	2109
CCA CTT A	ACA T Thr P 630	TT (GCA :	AAT Asn	Ala	GAT Asp 635	TCA Ser	GGT Gly	TTA Leu	Leu	CAT His 640	TCT Ser	TCT Ser	GTG Val	2157
AAA AGA A Lys Arg S	AGC T Ser C	GT 1 ys S	CA (Ser (CAG	AAT Asn	GAT Asp	TCT Ser	GAA Glu	GAA Glu	CCA Pro	ACT Thr	TTG Leu	TCC Ser	TTA Leu	2205

	645	•				650)				655	5				
ACT Thr 660	Ser	TCT Ser	TTT Phe	r GGC e Gl _y	ACA Thr	Ile	CTC	3 AGG 1 Arg	AAA Lys	A TGT 670	s Ser	AGA Arc	A AAT J Asr	GAZ Glu	A ACA Thr 675	2253
TGT Cys	TCT Ser	' AAT ' Asn	AAT Asr	ACA Thr	· Val	ATC Ile	: TCI	CAG	GAT Asp 685	Let	GAT Asp	TAT Tyr	AAA Lys	GAA Glu	GCA Ala	2301
AAA Lys	TGT Cys	AAT Asn	AAG Lys 695	Glu	AAA Lys	CTA Leu	CAG Gln	TTA Leu 700	Phe	ATT	ACC Thr	CCA Pro	GAA Glu 705	Ala	GAT Asp	2349
TCT Ser	CTG Leu	TCA Ser 710	Cys	CTG Leu	CAG Gln	GAA Glu	GGA Gly 715	. CAG Gln	TGT Cys	' GAA Glu	AAT Asn	GAT Asp	Pro	AAA Lys	AGC Ser	2397
AAA Lys	AAA Lys 725	GTT Val	TCA Ser	GAT Asp	ATA Ile	AAA Lys 730	GAA Glu	GAG Glu	GTC Val	TTG Leu	GCT Ala 735	GCA Ala	GCA Ala	TGT Cys	CAC His	2445
CCA Pro 740	GTA Val	CAA Gln	CAT His	TCA Ser	AAA Lys 745	GTG Val	GAA Glu	TAC Tyr	AGT Ser	GAT Asp 750	ACT Thr	GAC Asp	TTT Phe	CAA Gln	TCC Ser 755	2493
CAG Gln	AAA Lys	AGT Ser	CTT Leu	TTA Leu 760	TAT Tyr	GAT Asp	CAT His	GAA Glu	AAT Asn 765	GCC Ala	AGC Ser	ACT Thr	CTT Leu	ATT Ile 770	TTA Leu	2541
ACT Thr	CCT Pro	ACT Thr	TCC Ser 775	AAG Lys	GAT Asp	GTT Val	CTG Leu	TCA Ser 780	AAC Asn	CTA Leu	GTC Val	ATG Met	ATT Ile 785	TCT Ser	AGA Arg	2589
GGC Gly	AAA Lys	GAA Glu 790	TCA Ser	TAC Tyr	AAA Lys	ATG Met	TCA Ser 795	GAC Asp	AAG Lys	CTC Leu	AAA Lys	GGT Gly 800	AAC Asn	AAT Asn	TAT Tyr	2637
GAA Glu	TCT Ser 805	GAT Asp	GTT Val	GAA Glu	TTA Leu	ACC Thr 810	AAA Lys	AAT Asn	ATT Ile	CCC Pro	ATG Met 815	GAA Glu	AAG Lys	AAT Asn	CAA Gln	2685
GAT Asp 820	GTA Val	TGT Cys	GCT Ala	TTA Leu	AAT Asn 825	GAA Glu	AAT Asn	TAT Tyr	AAA Lys	AAC Asn 830	GTT Val	GAG Glu	CTG Leu	TTG Leu	CCA Pro 835	2733
CCT Pro	GAA Glu	AAA Lys	TAC Tyr	ATG Met 840	AGA Arg	GTA Val	GCA Ala	TCA Ser	CCT Pro 845	TCA Ser	AGA Arg	AAG Lys	GTA Val	CAA Gln 850	TTC Phe	2781
AAC Asn	CAA Gln	AAC Asn	ACA Thr	AAT Asn	CTA Leu	AGA Arq	GTA Val	ATC Ile	CAA Gln	AAA Lvs	AAT Asp	CAA Gln	GAA Glu	GAA Glu	ACT Thr	2829

Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr

AC:	r TC <i>l</i> r Sei	A ATT 116 870	e Ser	AAA Lys	A ATA	A ACT	GT(Va] 875	l Asn	CCA Pro	GAC Asp	C TCT Ser	GAA Glu 880	ı Glu	CTI Leu	TTC Phe	2877
TC/ Sei	A GAC Asp 885	Asr.	GAG Glu	AAT Asn	'AAT Asn	TTT Phe	· Val	TTC Phe	CAA Gln	GTA Val	GCT Ala 895	Asn	GAA Glu	AGG Arg	AAT Asn	2925
AAT Asr 900	ı Leu	GCT Ala	TTA Leu	GGA Gly	AAT Asn 905	Thr	' AAG	GAA Glu	CTT Leu	CAT His 910	Glu	ACA Thr	GAC Asp	TTG Leu	ACT Thr 915	2973
TGT Cys	GTA Val	AAC Asn	GAA Glu	CCC Pro 920	ATT Ile	TTC Phe	AAG Lys	AAC Asn	TCT Ser 925	ACC Thr	ATG Met	GTT Val	TTA Leu	TAT Tyr 930	GGA Gly	3021
GAC Asp	ACA Thr	GGT Gly	GAT Asp 935	AAA Lys	CAA Gln	GCA Ala	ACC Thr	CAA Gln 940	GTG Val	TCA Ser	ATT Ile	AAA Lys	AAA Lys 945	GAT Asp	TTG Leu	3069
GTT Val	TAT Tyr	GTT Val 950	CTT Leu	GCA Ala	GAG Glu	GAG Glu	AAC Asn 955	AAA Lys	AAT Asn	AGT Ser	GTA Val	AAG Lys 960	CAG Gln	CAT His	ATA Ile	3117
AAA Lys	ATG Met 965	ACT Thr	CTA Leu	GGT Gly	CAA Gln	GAT Asp 970	TTA Leu	AAA Lys	TCG Ser	GAC Asp	ATC Ile 975	TCC Ser	TTG Leu	AAT Asn	ATA Ile	3165
GAT Asp 980	AAA Lys	ATA Ile	CCA Pro	GAA Glu	AAA Lys 985	AAT Asn	AAT Asn	GAT Asp	TAC Tyr	ATG Met 990	AAC Asn	AAA Lys	TGG Trp	GCA Ala	GGA Gly 995	3213
CTC Leu	TTA Leu	GGT Gly	CCA Pro 1	ATT Ile .000	TCA Ser	AAT Asn	CAC His	Ser	TTT Phe	GGA Gly	GGT Gly	AGC Ser	Phe	AGA Arg	ACA Thr	3261
GCT Ala	TCA Ser	Asn	AAG Lys .015	GAA Glu	ATC Ile	AAG Lys	Leu	TCT Ser	GAA Glu	CAT His	AAC Asn	Ile	AAG Lys .025	AAG Lys	AGC Ser	3309
AAA Lys	Met	TTC Phe .030	TTC Phe	AAA Lys	GAT Asp	Ile	GAA Glu 035	GAA Glu	CAA Gln	TAT Tyr	Pro	ACT Thr 040	AGT Ser	TTA Leu	GCT Ala	3357
Cys	GTT Val .045	GAA Glu	ATT Ile	GTA Val	Asn	ACC Thr 050	TTG Leu	GCA Ala	TTA Leu	Asp .	AAT Asn 055	CAA Gln	AAG Lys	AAA Lys	CTG Leu	3405
AGC Ser	AAG Lys	CCT Pro	CAG '	TCA . Ser	ATT Ile	AAT Asn	ACT Thr	GTA '	TCT Ser .	GCA Ala :	CAT His	TTA Leu	CAG :	AGT Ser	AGT Ser	3453

1060	1065	1070	1075
GTA GTT GTT TCT Val Val Val Ser	I GAT TGT AAA AA: r Asp Cys Lys Ası 1080	F AGT CAT ATA ACC CCT n Ser His Ile Thr Pro 1085	CAG ATG TTA 3501 Gln Met Leu 1090
TTT TCC AAG CAC Phe Ser Lys Glr 1095	n Asp Phe Asn Sen	A AAC CAT AAT TTA ACA Asn His Asn Leu Thr 1100	CCT AGC CAA 3549 Pro Ser Gln
AAG GCA GAA ATT Lys Ala Glu Ile 1110	F ACA GAA CTT TCT Thr Glu Leu Ser 1115	T ACT ATA TTA GAA GAA Thr Ile Leu Glu Glu 1120	TCA GGA AGT 3597 Ser Gly Ser
CAG TTT GAA TTT Gln Phe Glu Phe 1125	C ACT CAG TTT AGA Thr Gln Phe Arg 1130	A AAA CCA AGC TAC ATA g Lys Pro Ser Tyr Ile 1135	TTG CAG AAG 3645 Leu Gln Lys
AGT ACA TTT GAA Ser Thr Phe Glu 1140	A GTG CCT GAA AAC 1 Val Pro Glu Asn 1145	CAG ATG ACT ATC TTA Gln Met Thr Ile Leu 1150	AAG ACC ACT 3693 Lys Thr Thr 1155
Ser Glu Glu Cys	AGA GAT GCT GAT Arg Asp Ala Asp 1160	CTT CAT GTC ATA ATG Leu His Val Ile Met 1165	AAT GCC CCA 3741 Asn Ala Pro 1170
TCG ATT GGT CAG Ser Ile Gly Gln 1175	Val Asp Ser Ser	AAG CAA TTT GAA GGT Lys Gln Phe Glu Gly 1180	ACA GTT GAA 3789 Thr Val Glu 185
ATT AAA CGG AAG Ile Lys Arg Lys 1190	TTT GCT GGC CTG Phe Ala Gly Leu 1195	TTG AAA AAT GAC TGT Leu Lys Asn Asp Cys 1200	AAC AAA AGT 3837 Asn Lys Ser
GCT TCT GGT TAT Ala Ser Gly Tyr 1205	TTA ACA GAT GAA Leu Thr Asp Glu 1210	AAT GAA GTG GGG TTT Asn Glu Val Gly Phe 1215	AGG GGC TTT 3885 Arg Gly Phe
TAT TCT GCT CAT Tyr Ser Ala His 1220	GGC ACA AAA CTG Gly Thr Lys Leu 1225	AAT GTT TCT ACT GAA (Asn Val Ser Thr Glu 2	GCT CTG CAA 3933 Ala Leu Gln 1235
Lys Ala Val Lys	CTG TTT AGT GAT Leu Phe Ser Asp 1240	ATT GAG AAT ATT AGT (Ile Glu Asn Ile Ser (1245	GAG GAA ACT 3981 Glu Glu Thr 1250
TCT GCA GAG GTA Ser Ala Glu Val 1255	His Pro Ile Ser	TTA TCT TCA AGT AAA T Leu Ser Ser Ser Lys (TGT CAT GAT 4029 Cys His Asp 265
TCT GTT GTT TCA Ser Val Val Ser	ATG TTT AAG ATA Met Phe Lys Ile	GAA AAT CAT AAT GAT A	AAA ACT GTA 4077 Lys Thr Val

AGT	GAA	AAA	AAT	' AAT	' AAA	TGC	CAA	CTG	ATA	TTA	CAA	AAT	' AAT	ATI	GAA	4125
261	1285		ASII	ASI	ггуя	1290		Leu	TTE	е ьет	1295 1295		. Asn	ı Ile	Glu	
ል ጥር	: дст	י אריידי	י ממר	י אכיד	ւ փար	· Cimm	C 7\ 7\	C 7 7	7 000	1 3 CH		70 70 FF	m* 0	. 7.7.0	AGA	
Met	Thr	Thr	Gly	Thr	Phe	Val	Glu	. GAA . Glu	Ile	Thr	GAA	AAT Asn	Tyr	Lys	AGA Arg	4173
1300					1305					1310			-	4	1315	
AAT	ACT	GAA	AAT	GAA	GAT	AAC	AAA	TAT	ACT	GCT	GCC	AGT	AGA	. AAT	TCT	4221
			Asn	Glu	Asp			Tyr	Thr	Ala					Ser	41
				1320					1325					1330		
CAI	AAC	TTA	GAA	TTT	GAT	GGC	AGT	GAT	TCA	AGT	' AAA	AAT	GAT	ACT	GTT	4269
His	Asn		GIu 1335	Phe	Asp	Gly		Asp 1340	Ser	Ser	Lys		Asp 1345	Thr	Val	
TGT Cvs	' ATT Ile	CAT	AAA	GAT	GAA	ACG Thr	GAC	TTG	CTA	TTT	ACT	GAT	CAG	CAC	AAC Asn	4317
- 1		1350	Lyb	, rob	OIU		1355	шеи	пеп	PHE		ASP 1360	GII	HIS	Asn	
ል ጥ ል	ጥርሞ	CTT	7\7\7\	יייים א	TUCTU	aaa	C7 C	an man	7 ma	770	a 7 a	~~~		- ~-	CAG	
Ile	Cys	Leu	Lys	Leu	Ser	Gly	Gln	Phe	Met	Lys	GAG	GGA	AAC Asn	ACT Thr	CAG Gln	4365
	1365					1370					1375	•				
ATT	AAA	GAA	GAT	TTG	TCA	GAT	TTA	ACT	TTT	TTG	GAA	GTT	GCG	AAA	GCT	4413
Ile				Leu	Ser			Thr	Phe	Leu						
1380					1385					1390					1395	
CAA	GAA	GCA	TGT	CAT	GGT	AAT	ACT	TCA	AAT	AAA	GAA	CAG	TTA	ACT	GCT	4461
GIN	GIU	Ата		H15	GIY	Asn	Thr	Ser	Asn 1405	Lys	Glu	Gln		Thr 1410	Ala	
ACT Thr	AAA Lvs	ACG Thr	GAG	CAA Gln	AAT Agn	ATA	AAA	GAT Asp	TTT	GAG	ACT	TCT	GAT	ACA	TTT	4509
	-2 -		L415	0.111	11011	110		1420	FIIC	Giu	TIIT		ASD 1425	THE	Pne	
TTT	CAG	аст	GCA	ልርጥ	GGG	73 73 73	አ አጥ	ATT	λСТ	CTT C	aaa	73. 73. 73.	G 7. G	TT C 7		
Phe	Gln	Thr	Ala	Ser	Gly	Lys	Asn	Ile	Ser	Val	Ala	Lys	GAG	Ser	TTT Phe	4557
		430					435					440				
AAT	AAA	ATT	GTA	AAT	TTC	TTT	GAT	CAG	AAA	CCA	GAA	GAA	TTG	CAT	AAC	4605
Asn	Lys	Ile	Val	Asn	Phe	Phe	Asp	Gln	Lys	Pro	Glu	Glu	Leu	His	Asn	
-	L445				1	.450]	L455					
TTT	TCC	TTA	AAT	TCT	GAA	TTA	CAT	TCT	GAC	ATA	AGA	AAG	AAC	AAA	ATG	4653
1460	ser	ьeu	asn		G1u .465	ьeu	HIS	Ser		Ile 470	Arg	Lys	Asn	_	Met L475	
CIA CI	7	O.T.	7 ~-													
Asp	Ile	Leu	AGT Ser	TAT	GAG Glu	GAA Glu	ACA Thr	GAC Asp	ATA Ile	GTT Val	AAA	CAC	AAA	ATA	CTG	4701

1685	1690	1695	
GGT CAA CCA GAA	AGA ATA AAT ACT	F GCA GAT TAT GTA (GGA AAT TAT TTG 5373
Gly Gln Pro Glu	Arg Ile Asn Thi	Ala Asp Tyr Val (Gly Asn Tyr Leu
1700	1705	1710	1715
Tyr Glu Asn Asn	TCA AAC AGT ACT	T ATA GCT GAA AAT 0	SAC AAA AAT CAT 5421
	Ser Asn Ser Thr	Tile Ala Glu Asn A	Asp Lys Asn His
	1720	1725	1730
CTC TCC GAA AAA	CAA GAT ACT TAT	TTA AGT AAC AGT A	GC ATG TCT AAC 5469
Leu Ser Glu Lys		Leu Ser Asn Ser S	Ser Met Ser Asn
1735		1740	1745
		G GTA TAT AAT GAT T Val Tyr Asn Asp S 17	
TCA AAA AAT AAA Ser Lys Asn Lys 1765	CTT GAT TCT GGT Leu Asp Ser Gly 1770	ATT GAG CCA GTA T Ile Glu Pro Val I 1775	TG AAG AAT GTT 5565 eu Lys Asn Val
GAA GAT CAA AAA	AAC ACT AGT TTT	TCC AAA GTA ATA T	CC AAT GTA AAA 5613
Glu Asp Gln Lys	Asn Thr Ser Phe	Ser Lys Val Ile S	er Asn Val Lys
1780	1785	1790	1795
Asp Ala Asn Ala	TAC CCA CAA ACT	GTA AAT GAA GAT A	TT TGC GTT GAG 5661
	Tyr Pro Gln Thr	Val Asn Glu Asp I	le Cys Val Glu
	1800	1805	1810
GAA CTT GTG ACT	Ser Ser Ser Pro	TGC AAA AAT AAA A	AT GCA GCC ATT 5709
Glu Leu Val Thr		Cys Lys Asn Lys A	sn Ala Ala Ile
1815		1820	1825
AAA TTG TCC ATA	TCT AAT AGT AAT	AAT TTT GAG GTA G	ly Pro Pro Ala
Lys Leu Ser Ile	Ser Asn Ser Asn	Asn Phe Glu Val G	
1830	1835	18	
TTT AGG ATA GCC Phe Arg Ile Ala 1845	AGT GGT AAA ATC Ser Gly Lys Ile 1850	GTT TGT GTT TCA C. Val Cys Val Ser H 1855	AT GAA ACA ATT 5805 is Glu Thr Ile
AAA AAA GTG AAA	GAC ATA TTT ACA	GAC AGT TTC AGT A	AA GTA ATT AAG 5853
Lys Lys Val Lys	Asp Ile Phe Thr	Asp Ser Phe Ser L	ys Val Ile Lys
1860	1865	1870	1875
Glu Asn Asn Glu	AAT AAA TCA AAA	ATT TGC CAA ACG AM	AA ATT ATG GCA 5901
	Asn Lys Ser Lys	Ile Cys Gln Thr Ly	/s Ile Met Ala
	880	1885	1890
GGT TGT TAC GAG	GCA TTG GAT GAT	TCA GAG GAT ATT CT	TT CAT AAC TCT 5949
Gly Cys Tyr Glu	Ala Leu Asp Asp	Ser Glu Asp Ile Le	

Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser

ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu

2100	2105	2110	2115
CAC TGT GTA A	AAC TCA GAA ATG GA	A AAA ACC TGC AGT A	AAA GAA TTT AAA 6621
	Asn Ser Glu Met Gl	u Lys Thr Cys Ser I	ays Glu Phe Lys
	2120	2125	2130
Leu Ser Asn A	AAC TTA AAT GTT GA	A GGT GGT TCT TCA G	AA AAT AAT CAC 6669
	Asn Leu Asn Val Gl	u Gly Gly Ser Ser G	lu Asn Asn His
	.35	2140	2145
TCT ATT AAA G	ETT TCT CCA TAT CT	C TCT CAA TTT CAA C	AA GAC AAA CAA 6717
Ser Ile Lys V	Val Ser Pro Tyr Le	u Ser Gln Phe Gln G	In Asp Lys Gln
2150	215	5 21	60
CAG TTG GTA T Gln Leu Val L 2165	TA GGA ACC AAA GT eu Gly Thr Lys Va 2170	C TCA CTT GTT GAG A l Ser Leu Val Glu A 2175	AC ATT CAT GTT 6765 sn Ile His Val
TTG GGA AAA G	AA CAG GCT TCA CC	T AAA AAC GTA AAA A	TG GAA ATT GGT 6813
Leu Gly Lys G	lu Gln Ala Ser Pr	o Lys Asn Val Lys M	et Glu Ile Gly
2180	2185	2190	2195
AAA ACT GAA A Lys Thr Glu T	CT TTT TCT GAT GT hr Phe Ser Asp Va 2200	T CCT GTG AAA ACA A l Pro Val Lys Thr A 2205	AT ATA GAA GTT 6861 sn Ile Glu Val 2210
TGT TCT ACT T	yr Ser Lys Asp Se:	A GAA AAC TAC TTT G	AA ACA GAA GCA 6909
Cys Ser Thr T		r Glu Asn Tyr Phe G	lu Thr Glu Ala
22:		2220	2225
GTA GAA ATT GO	CT AAA GCT TTT ATG	G GAA GAT GAT GAA C	eu Thr Asp Ser
Val Glu Ile A	la Lys Ala Phe Met	C Glu Asp Asp Glu Lo	
2230	2239	C 22	
AAA CTG CCA AG Lys Leu Pro Se 2245	GT CAT GCC ACA CAT er His Ala Thr His 2250	T TCT CTT TTT ACA TO S Ser Leu Phe Thr Cy 2255	GT CCC GAA AAT 7005 ys Pro Glu Asn
GAG GAA ATG GT	TT TTG TCA AAT TCA	A AGA ATT GGA AAA AG	GA AGA GGA GAG 7053
Glu Glu Met Va	al Leu Ser Asn Ser	Arg Ile Gly Lys An	Gg Arg Gly Glu
2260	2265	2270	2275
CCC CTT ATC TT Pro Leu Ile Le	TA GTG GGA GAA CCC eu Val Gly Glu Pro 2280	TCA ATC AAA AGA AA Ser Ile Lys Arg As 2285	AC TTA TTA AAT 7101 sn Leu Leu Asn 2290
GAA TTT GAC AG	g Ile Ile Glu Asn	CAA GAA AAA TCC TT	"A AAG GCT TCA 7149
Glu Phe Asp Ar		Gln Glu Lys Ser Le	eu Lys Ala Ser
229		2300	2305
AAA AGC ACT CC	A GAT GGC ACA ATA	AAA GAT CGA AGA TT	G TTT ATG CAT 7197
Lys Ser Thr Pr	Asp Gly Thr Ile	Lys Asp Arg Arg Le	u Phe Met His

CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG	7245
His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325 2330 2335	
2325 2330 2335	
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA	7293
Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu	, 233
2340 2345 2350 2355	
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT	
Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser	7341
2360 2365 2370	
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT	7389
Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375 2380 2385	
23/5 2380 2385	
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC	7437
Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr	
2390 2395 2400	
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT	
Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val	74.85
2405 2410 2415	
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA	7533
Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln 2420 2425 2430 2435	
2425 2430 2435	
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC	7581
Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp	
2440 2445 2450	
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA	7600
Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala	7629
2455 2460 2465	
CTA ACT MING ACA AND THE CAR CAR CAR CAR	
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT Val Thr Phe Thr Lys Cys Glu Glu Pro Leu Asp Leu Ile Thr Ser	7677
2470 2475 Led Asp Led The Thr Ser	
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA	7725
Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Gln	
2485 2490 2495	
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA	7773
Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr	1113
2500 2505 2510 2515	
TCC ACT CTC CCT ATC TCT CTC TTC	
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val	7821
tree mys Ara Ara var Gry GIN val	

				2520					2525					2530		
CCC Pro	: TCT	GCG Ala	TGT Cys 2535	TCT Ser	CAT His	AAA Lys	Gln	CTG Leu 2540	Tyr	ACG Thr	TAT	Gly	GTT Val 2545	TCT Ser	AAA Lys	7869
			Lys			Ser					Ser				CAC His	7917
Thr	GAA Glu 2565	Asp	TAT Tyr	TTT Phe	Gly	AAG Lys 2570	GAA Glu	AGT Ser	TTA Leu	Trp	ACT Thr 2575	GGA Gly	AAA Lys	GGA Gly	ATA Ile	7965
CAG Gln 2580	TTG Leu	GCT Ala	GAT Asp	Gly	GGA Gly 2585	TGG Trp	CTC Leu	ATA Ile	Pro	TCC Ser 2590	AAT Asn	GAT Asp	GGA Gly	Lys	GCT Ala 2595	8013
GGA Gly	AAA Lys	GAA Glu	Glu	TTT Phe 2600	TAT Tyr	AGG Arg	GCT Ala	Leu	TGT Cys 2605	GAC Asp	ACT Thr	CCA Pro	Gly	GTG Val 2610	GAT Asp	8061
CCA Pro	AAG Lys	CTT Leu	ATT Ile 2615	TCT Ser	AGA Arg	ATT Ile	Trp	GTT Val 2620	TAT Tyr	AAT Asn	CAC His	Tyr	AGA Arg 2625	TGG Trp	ATC Ile	8109
ATA Ile	Trp	AAA Lys 2630	CTG Leu	GCA Ala	GCT Ala	Met	GAA Glu 2635	TGT Cys	GCC Ala	TTT Phe	Pro	AAG Lys 2640	GAA Glu	TTT Phe	GCT Ala	8157
Asn	AGA Arg 2645	TGC Cys	CTA Leu	AGC Ser	Pro	GAA Glu 650	AGG Arg	GTG Val	CTT Leu	Leu	CAA Gln 2655	CTA Leu	AAA Lys	TAC Tyr	AGA Arg	8205
TAT Tyr 2660	GAT Asp	ACG Thr	GAA Glu	Ile	GAT Asp 2665	AGA Arg	AGC Ser	AGA Arg	Arg	TCG Ser 670	GCT Ala	ATA Ile	AAA Lys	Lys	ATA Ile 2675	8253
ATG Met	GAA Glu	AGG Arg	Asp	GAC Asp 680	ACA Thr	GCT Ala	GCA Ala	Lys	ACA Thr 685	CTT Leu	GTT Val	CTC Leu	Cys	GTT Val	TCT Ser	8301
GAC Asp	ATA Ile	ATT Ile	TCA Ser 695	TTG Leu	AGC Ser	GCA Ala	Asn	ATA Ile 700	TCT Ser	GAA Glu	ACT Thr	Ser	AGC Ser 705	AAT Asn	AAA Lys	8349
ACT Thr	Ser	AGT Ser 2710	GCA Ala	GAT Asp	ACC Thr	Gln	AAA Lys 715	GTG Val	GCC Ala	ATT Ile	Ile	GAA Glu 720	CTT Leu	ACA Thr	GAT Asp	8397
GGG Gly	TGG Trp	TAT Tyr	GCT Ala	GTT Val	AAG Lys	GCC Ala	CAG Gln	TTA Leu	GAT Asp	CCT Pro	CCC Pro	CTC Leu	TTA Leu	GCT Ala	GTC Val	8445

	2725					2730					2735					
				Arg					Gln		Ile			His	GGA Gly 2755	8493
			Val		TCT Ser			Ala					Glu		CCA Pro	8541
GAA Glu	TCT Ser	Leu	ATG Met 2775	TTA Leu	AAG Lys	ATT Ile	Ser	GCT Ala 2780	AAC Asn	AGT Ser	ACT Thr	Arg	CCT Pro 2785	GCT Ala	CGC Arg	8589
TGG Trp	Tyr	ACC Thr 2790	AAA Lys	CTT Leu	GGA Gly	Phe	TTT Phe 2795	CCT Pro	GAC Asp	CCT Pro	Arg	CCT Pro 2800	TTT Phe	CCT Pro	CTG Leu	8637
Pro	TTA Leu 2805	TCA Ser	TCG Ser	CTT Leu	TTC Phe	AGT Ser 2810	GAT Asp	GGA Gly	GGA Gly	Asn	GTT Val 2815	GGT Gly	TGT Cys	GTT Val	GAT Asp	8685
				Arg	GCA Ala 2825				Gln					Thr		8733
			Tyr		TTT Phe			Glu					Lys			8781
GCA Ala	AAA Lys	Tyr	GTG Val 2855	GAG Glu	GCC Ala	CAA Gln	Gln	AAG Lys 2860	AGA Arg	CTA Leu	GAA Glu	Ala	TTA Leu 865	TTC Phe	ACT Thr	8829
AAA Lys	Ile	CAG Gln 2870	GAG Glu	GAA Glu	TTT Phe	Glu	GAA Glu 875	CAT His	GAA Glu	GAA Glu	Asn	ACA Thr 880	ACA Thr	AAA Lys	CCA Pro	8877
Tyr	TTA Leu 885	CCA Pro	TCA Ser	CGT Arg	GCA Ala 2	CTA Leu 890	ACA Thr	AGA Arg	CAG Gln	Gln	GTT Val 895	CGT Arg	GCT Ala	TTG Leu	CAA Gln	8925
GAT Asp 2900	GGT Gly	GCA Ala	GAG Glu	Leu	TAT Tyr 1905	GAA Glu	GCA Ala	GTG Val	Lys	AAT Asn 910	GCA Ala	GCA Ala	GAC Asp	Pro	GCT Ala 915	8973
TAC Tyr	CTT Leu	GAG Glu	Gly	TAT Tyr 920	TTC Phe	AGT Ser	GAA Glu	Glu	CAG Gln 925	TTA Leu	AGA Arg	GCC Ala	Leu	AAT Asn 930	AAT Asn	9021

9069

CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA

His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu

Ile			Ala	Met	Glu				Gln	Lys			_	Leu	Ser	2117
		2950					2955					2960				
															AAA	9165
	Asp 2965	Val	Thr	Thr		Trp 2970	гуз	Leu	Arg		∨a⊥ 2975	Ser	Tyr	Ser	Lys	
AAA	GAA	ΔΑΔ	САТ	тса	GTT	מיד מ	ርጥር	ΣСТ	יוייני ∑	ጥርር	ССТ	CCA	ጥሮአ	ጥርአ	GAT	0212
		Lys														9213
2980					2985					2990					2995	
		TCT														9261
Leu	Tyr	Ser		Leu 3000	Thr	Glu	Gly		Arg 3005	Tyr	Arg	Ile		His 3010	Leu	
			•	5000					3003					3010		
		TCA														9309
Ala	TILL	Ser	ьув 3015	ser	гЛя	ser		Ser 3020	GIU	Arg	Ala		Ile 3025	GIn	Leu	
		ACA														9357
Ala		Thr 3030	пув	пув	THE		1yr 3035	Gin	GIN	ьeu		vaı 3040	Ser	Asp	GLu	
		TTT														9405
	ьеи 3045	Phe	GIN	iie		GIN 3050	Pro	Arg	Glu		Leu 3055	His	Phe	Ser	Lys	
					-	,,,,				•	,0,5					
		GAT														9453
9ne 3060	Leu	Asp	Pro		Pne 3065	GIn	Pro	Ser		Ser 3070	Glu	Val	Asp		Ile 3075	
				•				,	Ì	,0,0				•	3075	
		GTC														9501
GTÀ	Pne	Val		Ser 3080	Val	Val	Lys		Thr 3085	Gly	Leu	Ala		Phe 3090	Val	
								-	,005				•	3030		
		TCA														9549
Tyr	Leu	Ser	Asp 3095	GIu	Cys	Tyr		Leu 3100	Leu	Ala	Ile		Phe 3105	Trp	Ile	
		`	,0,5				`	7100				~	,105			
GAC	CTT	AAT	GAG	GAC	ATT	ATT	AAG	CCT	CAT	ATG	TTA	ATT	GCT	GCA	AGC	9597
Asp		Asn 3110	GIu	Asp	Ile		Lys 3115	Pro	His	Met		Ile 120	Ala	Ala	Ser	
	-	,,,,				_	,110					120				
		CAG														9645
	ьеи 3125	Gln	Trp	Arg		GLu 130	Ser	Lys	Ser		Leu 135	Leu	Thr	Leu	Phe	
_											. 1. 3					
GCT	GGA	GAT	TTT	TCT	GTG	TTT	TCT	GCT	AGT	CCA	AAA	GAG	GGC	CAC	TTT	9693
А⊥а	GLY	Asp	Phe	Ser	Val	Phe	Ser	Ala	Ser	Pro	Lys	Glu	Gly	His	Phe	

3140	3145	3150	3155
		AAA AAT ACT GTT GAG Lys Asn Thr Val Glu 3165	
Leu Cys Asn (AAG CTT ATG CAT ATA Lys Leu Met His Ile 3180	
GAT CCC AAG 1 Asp Pro Lys 1 3190	Trp Ser Thr Pro	ACT AAA GAC TGT ACT Thr Lys Asp Cys Thr 3195	TCA GGG CCG TAC 9837 Ser Gly Pro Tyr 200
ACT GCT CAA A Thr Ala Gln 1 3205	ATC ATT CCT GGT Ile Ile Pro Gly 3210	ACA GGA AAC AAG CTT Thr Gly Asn Lys Leu 3215	CTG ATG TCT TCT 9885 Leu Met Ser Ser
		CAA AGT CCT TTA TCA Gln Ser Pro Leu Ser 3230	
AAA AGG AAG I Lys Arg Lys S	TCT GTT TCC ACA Ser Val Ser Thr 3240	CCT GTC TCA GCC CAG Pro Val Ser Ala Gln 3245	ATG ACT TCA AAG 9981 Met Thr Ser Lys 3250
Ser Cys Lys G		ATT GAT GAC CAA AAG Ile Asp Asp Gln Lys 3260	
	eu Asp Phe Leu	AGT AGA CTG CCT TTA Ser Arg Leu Pro Leu 275	
AGT CCC ATT T Ser Pro Ile C 3285	GT ACA TTT GTT ys Thr Phe Val 3290	TCT CCG GCT GCA CAG Ser Pro Ala Ala Gln 3295	AAG GCA TTT CAG 10125 Lys Ala Phe Gln
CCA CCA AGG A Pro Pro Arg S 3300	GT TGT GGC ACC er Cys Gly Thr 3305	AAA TAC GAA ACA CCC . Lys Tyr Glu Thr Pro 3310	ATA AAG AAA AAA 10173 Ile Lys Lys 3315
GAA CTG AAT T Glu Leu Asn S	CT CCT CAG ATG . er Pro Gln Met . 3320	ACT CCA TTT AAA AAA ' Thr Pro Phe Lys Lys : 3325	TTC AAT GAA ATT 10221 Phe Asn Glu Ile 3330
TCT CTT TTG G Ser Leu Leu G 33:	lu Ser Asn Ser	ATA GCT GAC GAA GAA (Ile Ala Asp Glu Glu I 3340	CTT GCA TTG ATA 10269 Leu Ala Leu Ile 3345
AAT ACC CAA GO Asn Thr Gln A	CT CTT TTG TCT (la Leu Leu Ser (GGT TCA ACA GGA GAA A Gly Ser Thr Gly Glu I	AAA CAA TTT ATA 10317 Lys Gln Phe Ile

3350 3355 3360

TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT

Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr

3365 3370 3375

CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
3380 3395 3390 3395

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA Ile Thr Thr Lys Lys Tyr Ile 3415

10485

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe 25 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile 75 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys 85 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp 125 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val 135 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val 155

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Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
                 165
Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
                                 185
 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
                             200
                                                 205
 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
                         215
                                             220
Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
                    230
                                         235
Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
                245
                                     250
Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
                                 265
Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
                             280
Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
                         295
Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
                    310
                                         315
Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
                325
                                     330
Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
                                 345
Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
                            360
                                                 365
Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
                        375
                                             380
Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
                    390
                                        395
Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
                405
                                    410
Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
                                425
Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
                            440
Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
                        455
                                             460
Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
                    470
                                        475
Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
                485
                                    490
Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
            500
                                505
Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
                            520
Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
                                            540
Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
                    550
Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
                565
                                    570
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Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
            580
                                 585
Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
                             600
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
                         615
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
                     630
                                         635
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
                                     650
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
            660
                                 665
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
                             680
                                                685
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
                        695
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
                    710
                                         715
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
                                     730
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
            740
                                745
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
                            760
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
                        775
                                             780
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
                    790
                                        795
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
                805
                                     810
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
            820
                                825
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
                            840
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
                        855
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
                    870
                                        875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
                885
                                    890
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
            900
                                905
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
                            920
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
                        935
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
                    950
                                        955
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
                965
                                    970
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
                                985
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Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
        995
                            1000
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
                        1015
                                            1020
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
                     1030
                                        1035
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
                1045
                                    1050
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
            1060
                               1065
                                                    1070
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
                            1080
                                      1085
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
                        1095
                                           1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
                    1110
                                      1115
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
                1125
                                    1130
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
            1140
                                1145
                                                    1150
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
        1155
                            1160
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
                       1175
                                            1180
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
                    1190
                                       1195
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
                1205
                                   1210
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
            1220
                               1225
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
                            1240
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Lys
                        1255
                                            1260
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
                    1270
                                       1275
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
                                   1290
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
            1300
                               1305
                                                   1310
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
                           1320
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
                       1335
                                           1340
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
                    1350
                                       1355
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
                                   1370
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
            1380
                              1385
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
        1395
                           1400
                                               1405
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Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
    1410
                       1415
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
                   1430
                                       1435
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
                1445
                                   1450
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
            1460
                              1465
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
                          1480
                                              1485
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
                       1495
                                          1500
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
                   1510
                             1515
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
               1525
                                  1530
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
                               1545
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
                           1560
                                              1565
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
    1570
                       1575 1580
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
                  1590
                                      1595
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
               1605
                                  1610
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
                              1625
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
                           1640
                                              1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
                       1655
                                          1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
                   1670
                                      1675
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
               1685
                                  1690
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
           1700
                              1705
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
       1715
                1720
                                             1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
                      1735
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
                  1750
                                      1755
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
               1765
                                  1770
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
           1780
                              1785
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
       1795
                          1800
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
                       1815
                                          1820
```

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Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
                    1830
                                         1835
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
                 1845
                                     1850
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
             1860
                                 1865
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
                            1880
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
                        1895
                                            1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
                    1910
                                        1915
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
                1925
                                    1930
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
            1940
                                1945
                                                    1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
                            1960
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
                        1975
                                            1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
                    1990
                                        1995
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
                2005
                                    2010
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
            2020
                                2025
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
                            2040
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
                        2055
                                            2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
                    2070
                                        2075
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
                2085
                                    2090
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
            2100
                               2105
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
                            2120
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
                       2135
                                            2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
                   2150
                                       2155
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
                2165
                                    2170
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
            2180
                               2185
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
        2195
                           2200
                                                2205
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
                       2215
                                            2220
Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
                                       2235
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				224	5				225	0				Thr 225	5
Pro	Glu	Asn	Glu	Glu	Met	Val	Leu	Ser	Asn	Ser	Aro	ılle	Glv	Lys	Arc
			226	0				226	5				227	0	
Arg	GIY	G1u 227		Leu	Ile	Leu	Val 228		Glu	Pro	Ser	lle 228		Arg	Asr
T.e.i	T.e.	Aen	Glin	Dho	7 an	71 200			α1	7	~1			_	-
пса	229		Giu	. Phe	Asp	229	тте 5	ııre	GIU	Asn	230		Lys	Ser	Leu
Lys	Ala	Ser	Lys	Ser	Thr	Pro	Asp	Glv	Thr	Tle			Δτα	Arg	T.e.
230	5		4		231		1101	1		231		тър	Arg	vr. a	232
Phe	Met	His	Hig	Val			G] 11	Dro	Tla			1701	D-0-	Phe	202
				232		шси	U.L.u	FIO			Cys	vaı	PLO		
Thr	The	T	a 1			G 3	- 7	~7	233		_		_	233	
TIII	TIIT	пув	234		GII	GIU	тте	G1n 234		Pro	Asn	Phe	Thr 235	Ala 0	Pro
Gly	Gln	Glu	Phe	Leu	Ser	Lvs	Ser	His	Leu	Tvr	Glu	His	Len	Thr	Len
_		235	5			4	236			-1-		236			шСи
Glu	Lvs			Ser	Δan	T.e.1			Car	C1.	uic			Tyr	a 1
	237			DCI	11011	237		vai	Der	Gry			PILE	TAT	GII
17a T			mb.~	7 70 00	7 ~~			24 - 4-		'	238				
238		Ата	TIIT	Arg	239		гуѕ	мес	Arg	H15		lle	Thr	Thr	Gly 240
Arg	Pro	Thr	Lys	Val	Phe	Val	Pro	Pro	Phe	Lys	Thr	Lvs	Ser	His	Phe
				240					241					241	
His	Arq	Val	Glu	Gln	Cvs	Val	Ara	Asn			T.e.11	Glu	Glu	Asn	o Nra
			242	0	-1-		5	242		11011	шси	OIU	243		ALG
Gln	Lvs	Gln			Agn	Glaz	ui a			7 ~~	70	G	243	o Asn	-
0111		243!		110	App	GIY	244		ser	Asp	Asp			Asn	гда
T10	7 an			~~·	~~ T _	TT-1		-	_	_	_	244.			
116			ASII	GLU	тте			Pne	Asn	гЛа			Ser	Asn	Gln
70.7	2450			_,		245					246				
		Ата	val	Thr			Lys	Cys	Glu	Glu	Glu	Pro	Leu	Asp	Leu
2465					2470					2475					248
Ile	Thr	Ser	Leu	Gln	Asn	Ala	Arg	Asp	Ile	Gln	Asp	Met	Arg	Ile	Lys
				2485					249					2495	5
Lys	Lys	Gln	Arg	${\tt Gln}$	Arg	Val	Phe	Pro	Gln	Pro	Gly	Ser	Leu	Tyr	Leu
			2500					250!			_		2510		
Ala	Lys	Thr	Ser	Thr	Leu	Pro	Arq	Ile	Ser	Leu	Lvs	Ala	Ala	Val	Glv
		2515	5				2520					2525			- 1
Gly	Gln	Val	Pro	Ser	Ala	Cvs			Live	Gln	T.em			Tyr	C7.77
-	2530)				2535			-175	0111	254		1111	туг	Сту
Val			нiс	Cve				7) an	Cox	Tira			a1	Ser	1
2545		шув	1120	Cys			TTC	ASII	per			Ата	GIU	ser	
		774 -	ml	a1	2550		-1		_	2555					256
GIII	PHE	HIS	THE	2565	Asp	Tyr	Phe	GIA	Lуs 257(Ser	Leu	Trp	Thr 2575	
Lys	Gly	Ile	Gln	Leu	Ala	Asp	Glv	Glv	Trp	Leu	Tle	Pro	Ser	Asn	Δan
			2580)		-	-	2585		•			2590		тър
Glv	Lvs	Ala	Glv	Lvs	GIn	Glu	Dhe			717	Tou	Crra		Thr	D
		2595	1	-2-	Oiu	O.L.u	2600		ALG	ALA	цец			THE	Pro
Glv	Va l			Tare	T 011	тло			т1.		**- 7	2605		~~ 1	_
O I Y	761A	Asp	PIU	цуъ				Arg	тте	Trp			Asn	His	Tyr
	2610		T7 -	Шас		2615					2620				
erta	rrp	тте	тте	rrp			ALa	Ala	Met			Ala	Phe	Pro	Lys
2625 ~-				_	2630					2635					264
31u	Phe	Ala	Asn	Arg	Cys	Leu	Ser	Pro	Glu	Arg	Val	Leu	Leu	Gln	Leu
				2645					2650					2655	

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Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Ser Ala Ile
           2660
                               2665
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
                           2680
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
                        2695
                                           2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
                    2710
                                      2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
               2725
                                   2730
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
            2740
                   2745
                                                  2750
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
                           2760
                                              2765
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
                       2775
                                          2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
                   2790
                                       2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
                2805
                                   2810
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
                   2825
           2820
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu
                           2840
                                               2845
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
                       2855
                                          2860
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
                   2870
                                      2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
               2885
                                  2890
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
           2900
                               2905
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
                           2920
                                              2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
                       2935
                                          2940
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
                  2950
                                      2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
               2965
                                   2970
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
           2980
                              2985
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
       2995
                          3000
                                              3005
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
                       3015
                                          3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
                   3030
                                      3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
               3045
                                  3050
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
                              3065
                                                  3070
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Asp	neu	307		Pne	val	vai	308		. Val	. Lys	Lys	Thr 308	Gly	Leu	ı Ala
Pro	Phe	Va 1	Tvr	Len	Ser	Δen			Тз гз	. 7	T 011	Tou	ι Ala	T1.	
	309	0				309	5				310	0			
Phe	Trp	Ile	Asp	Leu	Asn	Glu	Asp	Ile	Ile	Lys	Pro	His	Met	Leu	Ile
310	5				311	0				311					312
Ala	Ala	Ser	Asn	Leu 312	Gln 5	Trp	Arg	Pro	Glu 313	Ser	Lys	Ser	Gly		Lei
Thr	T 11	Dhe	Nlα			Dho	00	77-7			77 .	a	_	313	5
			314	0				314	5				Pro 315	0	
Gly	His	Phe	Gln	Glu	Thr	Phe	Asn	Lys	Met	Lys	Asn	Thr	Val	Glu	Ası
		315	5				316	0				316	5		
Ile	Asp	Ile	Leu	Cys	Asn	Glu	Ala	Glu	Asn	Tivs	Leu	Met	His	Tle	Lei
	317	0		_		317	5			-1-	318		1110	110	ше
His			Asp	Pro	Taye			Thr	Dro	mb x			Cys	III a	a
318	5		тър		319	v TTD	UCI	1111	FIO			Asp	Cys	THE	
		TT 170	mb	77-			~ 7	_	~ 7	319		_			320
GIY	PIO	туг	TIIL			тте	тте	Pro			GIA	Asn	Lys		
		_	_	320					321					321	5
Met	Ser	Ser	Pro	Asn	Cys	Glu	Ile	Tyr	Tyr	Gln	Ser	Pro	Leu	Ser	Let
			3220					322					3230	0	
Cys	Met	Ala	Lys	Arg	Lys	Ser	Val	Ser	Thr	Pro	Val	Ser	Ala	Gln	Met
		3235	5				3240	0				324	5		
Thr	Ser	Lys	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lvs	Agn
	3250)		_	-	325	5	2			326			_, _	2101
Cvs	Lvs	Lvs	Ara	Ara	Ala			Dhe	T.011				Pro	Т от	Draw
3265	- <i>y</i> -	-2-	5	9	3270		тор	LIIC	пец			пеп	PLO	neu	
		T=T	Car	Dro			mla sa	Db -	T7_ 7	3275	,	~ 7			328
FIO	FIO	vai	ser	200		Cys	Thr	Pue			Pro	Ala	Ala		
71 -	D1	~7	_	3285		_		_	3290					3295	5
Ата	Pne	GIN	Pro	Pro	Arg	Ser	Cys			Lys	Tyr	Glu	Thr	Pro	Ile
			3300					3305					3310)	
Lys	Lys	Lys	Glu	Leu	Asn	Ser	Pro	Gln	Met	\mathtt{Thr}	Pro	Phe	Lys	Lys	Phe
		3315	5				3320)				3325	5		
Asn	Glu	Ile	Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu
	3330	li .				3335					3340				
Ala	Leu	Ile	Asn	Thr	Gln			T ₁ e11	Ser	G13z	Ser	Thr	Gly	C111	Tira
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		Tle	Ser	17 = 1			C0~	mile se	7 200	mb a	, ,	D	Thr	~	336
J 1.11	1110	4.20	Der	var	PET	Giu	ser	TILL			Ата	Pro	Thr		
~7	70	re-	_	3365			_		3370					3375	5
±1u	Asp	Tyr	ьeu	Arg	Leu	Lys				Thr	Thr	Ser	Leu	Ile	Lys
			3380					3385					3390)	
3lu	Gln	Glu	Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys
		3395					3400	1			-	3405			4
3ln	Asp	Thr	Ile	Thr	Thr	Lys	Lys	Tyr	Ile						
	3410					3415		-							

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 229...10482
 - (D) OTHER INFORMATION: BRCA2 (OMI2)
- (ix) FEATURE:
 - (A) NAME/KEY: variation
 - (B) LOCATION: 3624
 - (D) OTHER INFORMATION: R = A or G. Xaa (amino acid position 1132) = Lys.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCT ACA	GCTG GATT	CGC TGT	CTCG GACC	GGTG GGCG	TC T	TTTG TTTT	CGGC TGTC	G GT A GC	GGGT TTAC	CGCC TCCG	GCC	'GGGA 'AAAA	GAA AAG A AT	GCGT AACT G CC t Pr	TGCGCC GAGGGG GCACCT T ATT o Ile	60 120 180 237
GGA Gly	TCC Ser 5	AAA Lys	GAG Glu	AGG Arg	CCA Pro	ACA Thr 10	TTT Phe	TTT Phe	GAA Glu	ATT	TTT Phe 15	AAG Lys	ACA Thr	CGC Arg	TGC Cys	285
AAC Asn 20	AAA Lys	GCA Ala	GAT Asp	TTA Leu	GGA Gly 25	CCA Pro	ATA Ile	AGT Ser	CTT Leu	AAT Asn 30	TGG Trp	TTT Phe	GAA Glu	GAA Glu	CTT Leu 35	333
TCT Ser	TCA Ser	GAA Glu	GCT Ala	CCA Pro 40	CCC Pro	TAT Tyr	AAT Asn	TCT Ser	GAA Glu 45	CCT Pro	GCA Ala	GAA Glu	GAA Glu	TCT Ser 50	GAA Glu	381
CAT His	AAA Lys	AAC Asn	AAC Asn 55	AAT Asn	TAC Tyr	GAA Glu	CCA Pro	AAC Asn 60	CTA Leu	TTT	AAA Lys	ACT Thr	CCA Pro 65	CAA Gln	AGG Arg	429
AAA Lys	CCA Pro	TCT Ser 70	TAT Tyr	AAT Asn	CAG Gln	CTG Leu	GCT Ala 75	TCA Ser	ACT Thr	CCA Pro	ATA Ile	ATA Ile 80	TTC Phe	AAA Lys	GAG Glu	477
CAA Gln	GGG Gly 85	CTG Leu	ACT Thr	CTG Leu	CCG Pro	CTG Leu 90	TAC Tyr	CAA Gln	TCT Ser	CCT Pro	GTA Val 95	AAA Lys	GAA Glu	TTA Leu	GAT Asp	525
AAA Lys 100	TTC Phe	AAA Lys	TTA Leu	GAC Asp	TTA Leu 105	GGA Gly	AGG Arg	AAT Asn	GTT Val	CCC Pro 110	AAT Asn	AGT Ser	AGA Arg	CAT His	AAA Lys 115	573
AGT Ser	CTT Leu	CGC Arg	ACA Thr	GTG Val 120	AAA Lys	ACT Thr	AAA Lys	ATG Met	GAT Asp 125	CAA Gln	GCA Ala	GAT Asp	GAT Asp	GTT Val 130	TCC Ser	621

				Asn					Glu					Leu	CAA Gln	669
			Val					Asp			GTG Val		Cys			717
TTG Leu	TTT Phe 165	CAT	' ACA Thr	CCA Pro	AAG Lys	TTT Phe 170	GTG Val	AAG Lys	GGT Gly	CGT Arg	CAG Gln 175	Thr	CCA Pro	AAA Lys	CAT	765
ATT Ile 180	TCT Ser	GAA Glu	AGT Ser	CTA Leu	GGA Gly 185	GCT Ala	GAG Glu	GTG Val	GAT Asp	CCT Pro 190	GAT Asp	ATG Met	TCT Ser	TGG Trp	TCA Ser 195	813
											ACT Thr					861
AGA Arg	AAT Asn	GAA Glu	GAA Glu 215	GCA Ala	TCT Ser	GAA Glu	ACT Thr	GTA Val 220	TTT Phe	CCT Pro	CAT His	GAT Asp	ACT Thr 225	ACT Thr	GCT Ala	909
AAT Asn	GTG Val	AAA Lys 230	AGC Ser	TAT Tyr	TTT Phe	TCC Ser	AAT Asn 235	CAT His	GAT Asp	GAA Glu	AGT Ser	CTG Leu 240	AAG Lys	AAA Lys	AAT Asn	957
GAT Asp	AGA Arg 245	TTT Phe	ATC Ile	GCT Ala	TCT Ser	GTG Val 250	ACA Thr	GAC Asp	AGT Ser	GAA Glu	AAC Asn 255	ACA Thr	AAT Asn	CAA Gln	AGA Arg	1005
GAA Glu 260	GCT Ala	GCA Ala	AGT Ser	CAT His	GGA Gly 265	TTT Phe	GGA Gly	AAA Lys	ACA Thr	TCA Ser 270	GGG Gly	AAT Asn	TCA Ser	TTT Phe	AAA Lys 275	1053
GTA Val	AAT Asn	AGC Ser	TGC Cys	AAA Lys 280	GAC Asp	CAC His	ATT Ile	GGA Gly	AAG Lys 285	TCA Ser	ATG Met	CCA Pro	AAT Asn	GTC Val 290	CTA Leu	1101
GAA Glu	GAT Asp	GAA Glu	GTA Val 295	TAT Tyr	GAA Glu	ACA Thr	GTT Val	GTA Val 300	GAT Asp	ACC Thr	TCT Ser	GAA Glu	GAA Glu 305	GAT Asp	AGT Ser	1149
											AAT Asn					1197
Arg	ACT Thr 325	AGC Ser	AAG Lys	ACT Thr	AGG Arg	AAA Lys 330	AAA Lys	ATT Ile	TTC Phe	CAT His	GAA Glu 335	GCA Ala	AAC Asn	GCT Ala	GAT Asp	1245

GAA Glu 340	Cys	GAA Glu	AAA Lys	TCT Ser	Lys 345	Asn	CAA Gln	GTG Val	AAA Lys	GAA Glu 350	Lys	TAC Tyr	TCA Ser	TTT Phe	GTA Val 355	1293
TCT Ser	' GAA Glu	GTG Val	GAA Glu	CCA Pro 360	AAT Asn	GAT Asp	ACT Thr	' GAT Asp	CCA Pro 365	TTA Leu	GAT Asp	TCA Ser	AAT Asn	GTA Val 370	GCA Ala	1341
CAT His	CAG Gln	AAG Lys	Pro 375	TTT Phe	GAG Glu	AGT Ser	GGA Gly	AGT Ser 380	GAC Asp	AAA Lys	ATC Ile	TCC Ser	AAG Lys 385	GAA Glu	GTT Val	1389
			TTG Leu													1437
AAT Asn	GGA Gly 405	GCC Ala	CAG Gln	ATG Met	GAG Glu	AAA Lys 410	ATA Ile	CCC Pro	CTA Leu	TTG Leu	CAT His 415	ATT Ile	TCT Ser	TCA Ser	TGT Cys	1485
GAC Asp 420	CAA Gln	AAT Asn	ATT	TCA Ser	GAA Glu 425	AAA Lys	GAC Asp	CTA Leu	TTA Leu	GAC Asp 430	ACA Thr	GAG Glu	AAC Asn	AAA Lys	AGA Arg 435	1533
AAG Lys	AAA Lys	GAT Asp	TTT Phe	CTT Leu 440	ACT Thr	TCA Ser	GAG Glu	AAT Asn	TCT Ser 445	TTG Leu	CCA Pro	CGT Arg	ATT Ile	TCT Ser 450	AGC Ser	1581
CTA Leu	CCA Pro	AAA Lys	TCA Ser 455	GAG Glu	AAG Lys	CCA Pro	TTA Leu	AAT Asn 460	GAG Glu	GAA Glu	ACA Thr	GTG Val	GTA Val 465	AAT Asn	AAG Lys	1629
AGA Arg	GAT Asp	GAA Glu 470	GAG Glu	CAG Gln	CAT His	CTT Leu	GAA Glu 475	TCT Ser	CAT His	ACA Thr	GAC Asp	TGC Cys 480	ATT Ile	CTT Leu	GCA Ala	1677
GTA Val	AAG Lys 485	CAG Gln	GCA Ala	ATA Ile	TCT Ser	GGA Gly 490	ACT Thr	TCT Ser	CCA Pro	GTG Val	GCT Ala 495	TCT Ser	TCA Ser	TTT Phe	CAG Gln	1725
GGT Gly 500	ATC Ile	AAA Lys	AAG Lys	TCT Ser	ATA Ile 505	TTC Phe	AGA Arg	ATA Ile	AGA Arg	GAA Glu 510	TCA Ser	CCT Pro	AAA Lys	GAG Glu	ACT Thr 515	1773
TTC Phe	AAT Asn	GCA Ala	AGT Ser	TTT Phe 520	TCA Ser	GGT Gly	CAT His	ATG Met	ACT Thr 525	GAT Asp	CCA Pro	AAC Asn	TTT Phe	AAA Lys 530	AAA Lys	1821
GAA Glu	ACT Thr	GAA Glu	GCC Ala 535	TCT Ser	GAA Glu	AGT Ser	GGA Gly	CTG Leu 540	GAA Glu	ATA Ile	CAT His	ACT Thr	GTT Val 545	TGC Cys	TCA Ser	1869

CAG Gln	AAG Lys	GAC Glu 550	ı Asp	TCC Ser	TTA Leu	TGT Cys	Pro	Asn	TTA Leu	ATT	GAT Asp	AAT Asn 560	G1y	AGC Ser	TGG Trp	1917
CCA Pro	GCC Ala 565	Thr	ACC Thr	ACA Thr	CAG Gln	AAT Asn 570	TCT Ser	GTA Val	GCT Ala	'TTG Leu	AAG Lys 575	Asn	GCA Ala	GGT Gly	TTA Leu	1965
			TTG Leu								Ile					2013
GAT Asp	GAA Glu	ACA Thr	TCT Ser	TAT Tyr 600	AAA Lys	GGA Gly	AAA Lys	AAA Lys	ATA Ile 605	CCG Pro	AAA Lys	GAC Asp	CAA Gln	AAA Lys 610	TCA Ser	2061
			AAC Asn 615													2109
			TTT Phe													2157
AAA Lys	AGA Arg 645	AGC Ser	TGT Cys	TCA Ser	CAG Gln	AAT Asn 650	GAT Asp	TCT Ser	GAA Glu	GAA Glu	CCA Pro 655	ACT Thr	TTG Leu	TCC Ser	TTA Leu	2205
ACT Thr 660	AGC Ser	TCT Ser	TTT Phe	GGG Gly	ACA Thr 665	ATT Ile	CTG Leu	AGG Arg	AAA Lys	TGT Cys 670	TCT Ser	AGA Arg	AAT Asn	GAA Glu	ACA Thr 675	2253
TGT Cys	TCT Ser	AAT Asn	AAT Asn	ACA Thr 680	GTA Val	ATC Ile	TCT Ser	CAG Gln	GAT Asp 685	CTT Leu	GAT Asp	TAT Tyr	AAA Lys	GAA Glu 690	GCA Ala	2301
AAA Lys	TGT Cys	AAT Asn	AAG Lys 695	GAA Glu	AAA Lys	CTA Leu	CAG Gln	TTA Leu 700	TTT Phe	ATT Ile	ACC Thr	CCA Pro	GAA Glu 705	GCT Ala	GAT Asp	2349
TCT Ser	CTG Leu	TCA Ser 710	TGC Cys	CTG Leu	CAG Gln	GAA Glu	GGA Gly 715	CAG Gln	TGT Cys	GAA Glu	AAT Asn	GAT Asp 720	CCA Pro	AAA Lys	AGC Ser	2397
AAA Lys	AAA Lys 725	GTT Val	TCA Ser	GAT Asp	ATA Ile	AAA Lys 730	GAA Glu	GAG Glu	GTC Val	TTG Leu	GCT Ala 735	GCA Ala	GCA Ala	TGT Cys	CAC His	2445
CCA Pro 740	GTA Val	CAA Gln	CAT His	TCA Ser	AAA Lys 745	GTG Val	GAA Glu	TAC Tyr	AGT Ser	GAT Asp 750	ACT Thr	GAC Asp	TTT Phe	CAA Gln	TCC Ser 755	2493

															TTA Leu	2541
															AGA Arg	2589
			Ser												TAT Tyr	2637
															CAA Gln	2685
			GCT Ala													2733
			TAC Tyr													2781
AAC Asn	CAA Gln	AAC Asn	ACA Thr 855	AAT Asn	CTA Leu	AGA Arg	GTA Val	ATC Ile 860	CAA Gln	AAA Lys	AAT Asn	CAA Gln	GAA Glu 865	GAA Glu	ACT Thr	2829
ACT Thr	TCA Ser	ATT Ile 870	TCA Ser	AAA Lys	ATA Ile	ACT Thr	GTC Val 875	AAT Asn	CCA Pro	GAC Asp	TCT Ser	GAA Glu 880	GAA Glu	CTT Leu	TTC Phe	2877
			GAG Glu													2925
			TTA Leu													2973
TGT Cys	GTA Val	AAC Asn	GAA Glu	CCC Pro 920	ATT Ile	TTC Phe	AAG Lys	AAC Asn	TCT Ser 925	ACC Thr	ATG Met	GTT Val	TTA Leu	TAT Tyr 930	GGA Gly	3021
GAC Asp	ACA Thr	GGT Gly	GAT Asp 935	AAA Lys	CAA Gln	GCA Ala	ACC Thr	CAA Gln 940	GTG Val	TCA Ser	ATT Ile	AAA Lys	AAA Lys 945	GAT Asp	TTG Leu	3069
GTT Val	TAT Tyr	GTT Val 950	CTT Leu	GCA Ala	GAG Glu	GAG Glu	AAC Asn 955	AAA Lys	AAT Asn	AGT Ser	GTA Val	AAG Lys 960	CAG Gln	CAT His	ATA Ile	3117

AAA ATG ACT C Lys Met Thr L 965	CTA GGT CAA GA eu Gly Gln As 97	sp Leu Lys Se	G GAC ATC TCC T r Asp Ile Ser L 975	TG AAT ATA eu Asn Ile	3165
GAT AAA ATA C Asp Lys Ile P 980	CCA GAA AAA AA Pro Glu Lys As 985	T AAT GAT TA n Asn Asp Ty	C ATG AAC AAA T r Met Asn Lys T 990	GG GCA GGA rp Ala Gly 995	3213
CTC TTA GGT C Leu Leu Gly P	CA ATT TCA AA ro Ile Ser As 1000	T CAC AGT TT n His Ser Ph 100	T GGA GGT AGC T e Gly Gly Ser P 5	TC AGA ACA ne Arg Thr 1010	3261
	ys Glu Ile Ly		A CAT AAC ATT A u His Asn Ile L 102	ys Lys Ser	3309
AAA ATG TTC T Lys Met Phe P 1030	TC AAA GAT AT he Lys Asp Il	T GAA GAA CA e Glu Glu Gl 1035	A TAT CCT ACT AC n Tyr Pro Thr Se 1040	GT TTA GCT er Leu Ala	3357
TGT GTT GAA A' Cys Val Glu I 1045	TT GTA AAT AC le Val Asn Th 105	r Leu Ala Le	A GAT AAT CAA AA u Asp Asn Gln Ly 1055	AG AAA CTG 's Lys Leu	3405
AGC AAG CCT C Ser Lys Pro G 1060	AG TCA ATT AA ln Ser Ile As 1065	T ACT GTA TC n Thr Val Se	I GCA CAT TTA CA r Ala His Leu Gl 1070	AG AGT AGT n Ser Ser 1075	3453
GTA GTT GTT TO Val Val Val Se	CT GAT TGT AA er Asp Cys Ly 1080	A AAT AGT CA s Asn Ser Hi: 1089	F ATA ACC CCT CA S Ile Thr Pro Gl	AG ATG TTA n Met Leu 1090	3501
TTT TCC AAG CA Phe Ser Lys Gl 109	ln Asp Phe Ası	T TCA AAC CAT n Ser Asn His 1100	F AAT TTA ACA CO S Asn Leu Thr Pr 110	o Ser Gln	3549
AAG GCA GAA AT Lys Ala Glu II 1110	TT ACA GAA CT le Thr Glu Le	T TCT ACT ATA Ser Thr Ile 1115	A TTA GAA GAA TO E Leu Glu Glu Se 1120	A GGA AGT r Gly Ser	3597
CAG TTT GAA TT Gln Phe Glu Ph 1125	TT ACT CAG TT ne Thr Gln Phe 1130	e Arg Xaa Pro	AGC TAC ATA TT Ser Tyr Ile Le 1135	G CAG AAG u Gln Lys	3645
AGT ACA TTT GA Ser Thr Phe Gl 1140	AA GTG CCT GAA u Val Pro Glu 1145	A AAC CAG ATG A Asn Gln Met	ACT ATC TTA AA Thr Ile Leu Ly 1150	G ACC ACT s Thr Thr 1155	3693
TCT GAG GAA TG Ser Glu Glu Cy	GC AGA GAT GCT s Arg Asp Ala 1160	GAT CTT CAT Asp Leu His 1165	GTC ATA ATG AA	T GCC CCA n Ala Pro 1170	3741

TCG Ser	ATT	GGT Gly	CAG Gln 1175	Val	GAC Asp	AGC Ser	AGC Ser	AAG Lys 1180	Gln	TTT Phe	GAA	A GGT ı Gly	C ACA Thr 1185	. Val	GAA Glu	3789
ATT Ile	AAA Lys	. CGG Arg 1190	Lys	TTT Phe	GCT Ala	Gly	CTG Leu 1195	Leu	Lys	AAT Asn	GAC Asp	TGT Cys 1200	Asn	: AAA Lys	AGT Ser	3837
Ala	TCT Ser 1205	Gly	TAT Tyr	TTA Leu	Thr	GAT Asp 1210	GAA Glu	. AAT . Asn	GAA Glu	Val	GGG Gly 1215	Phe	' AGG Arg	GGC Gly	TTT	3885
TAT Tyr 1220	TCT Ser	GCT Ala	CAT	Gly	ACA Thr 1225	AAA Lys	CTG Leu	AAT Asn	Val	TCT Ser 1230	ACT Thr	GAA Glu	GCT Ala	Leu	CAA Gln 1235	3933
AAA Lys	GCT Ala	GTG Val	Lys	CTG Leu 1240	TTT Phe	AGT Ser	GAT Asp	Ile	GAG Glu 1245	AAT Asn	ATT Ile	AGT Ser	Glu	GAA Glu 1250	ACT Thr	3981
TCT Ser	GCA Ala	Glu	GTA Val 1255	CAT His	CCA Pro	ATA Ile	Ser	TTA Leu 1260	TCT Ser	TCA Ser	AGT Ser	Lys	TGT Cys 1265	CAT His	GAT Asp	4029
TCT Ser	Val	GTT Val 1270	TCA Ser	ATG Met	TTT Phe	Lys	ATA Ile L275	GAA Glu	AAT Asn	CAT His	Asn	GAT Asp 1280	AAA Lys	ACT Thr	GTA Val	4077
Ser	GAA Glu L285	AAA Lys	AAT Asn	AAT Asn	Lys	TGC Cys L290	CAA Gln	CTG Leu	ATA Ile	Leu	CAA Gln 1295	AAT Asn	AAT Asn	ATT Ile	GAA Glu	4125
ATG Met 1300	ACT Thr	ACT Thr	GGC Gly	Thr	TTT Phe L305	GTT Val	GAA Glu	GAA Glu	Ile	ACT Thr	GAA Glu	AAT Asn	TAC Tyr	AAG Lys	AGA Arg 1315	4173
AAT Asn	ACT Thr	GAA Glu	Asn	GAA Glu .320	GAT Asp	AAC Asn	AAA Lys	Tyr	ACT Thr	GCT Ala	GCC Ala	AGT Ser	Arg	AAT Asn L330	TCT Ser	4221
CAT His	AAC Asn	Leu	GAA Glu 335	TTT Phe	GAT Asp	GGC Gly	Ser	GAT Asp 340	TCA Ser	AGT Ser	AAA Lys	Asn	GAT Asp 345	ACT Thr	GTT Val	4269
TGT Cys	Ile	CAT His 350	AAA Lys	GAT Asp	GAA Glu	Thr .	GAC Asp 355	TTG Leu	CTA Leu	TTT Phe	\mathtt{Thr}	GAT Asp .360	CAG Gln	CAC His	AAC Asn	4317
Ile	TGT Cys 365	CTT Leu	AAA Lys	TTA Leu	Ser	GGC Gly 370	CAG Gln	TTT Phe	ATG Met	Lys	GAG Glu 375	GGA Gly	AAC Asn	ACT Thr	CAG Gln	4365

ATT Ile 1380	Lys	GAA Glu	GAT Asp	TTG Leu	TCA Ser 1385	Asp	' TTA Leu	ACI Thr	TTT	TTG Leu 1390	ı Glu	GTI Val	GCC Ala	a AAA Lys	GCT Ala 1395	4413
CAA Gln	GAA Glu	GCA Ala	Cys	CAT His	Gly	AAT Asn	ACT Thr	TCA Ser	AAT Asr 1405	Lys	GAA Glu	CAG Gln	TTA Leu	ACT Thr 1410	GCT Ala	4461
ACT Thr	AAA Lys	Thr	GAG Glu 1415	Gln	AAT Asn	ATA Ile	Lys	GAT Asp 1420	Phe	GAG Glu	ACT Thr	TCT	GAT Asp 1425	Thr	TTT	4509
TTT Phe	Gln	ACT Thr 1430	GCA Ala	AGT Ser	GGG Gly	Lys	AAT Asn 1435	ATT	AGT Ser	GTC Val	Ala	AAA Lys 1440	GAG Glu	TCA Ser	TTT Phe	4557
Asn	AAA Lys 1445	ATT Ile	GTA Val	AAT Asn	Phe	TTT Phe 1450	GAT Asp	CAG Gln	AAA Lys	Pro	GAA Glu 1455	GAA Glu	TTG Leu	CAT	AAC Asn	4605
TTT Phe 1460	TCC Ser	TTA Leu	AAT Asn	Ser	GAA Glu 1465	TTA Leu	CAT His	TCT Ser	Asp	ATA Ile 1470	AGA Arg	AAG Lys	AAC Asn	Lys	ATG Met 1475	4653
GAC Asp	ATT Ile	CTA Leu	Ser	TAT Tyr 1480	GAG Glu	GAA Glu	ACA Thr	Asp	ATA Ile 1485	GTT Val	AAA Lys	CAC His	Lys	ATA Ile 1490	CTG Leu	4701
AAA Lys	GAA Glu	Ser	GTC Val 495	CCA Pro	GTT Val	GGT Gly	Thr	GGA Gly .500	AAT Asn	CAA Gln	CTA Leu	Val	ACC Thr 1505	TTC Phe	CAG Gln	4749
GGA Gly	Gln	CCC Pro 510	GAA Glu	CGT Arg	GAT Asp	Glu	AAG Lys .515	ATC Ile	AAA Lys	GAA Glu	CCT Pro	ACT Thr	CTG Leu	TTG Leu	GGT Gly	4797
Phe	CAT His 525	ACA Thr	GCT Ala	AGC Ser	Gly	AAA Lys 530	AAA Lys	GTT Val	AAA Lys	Ile	GCA Ala L535	AAG Lys	GAA Glu	TCT Ser	TTG Leu	4845
GAC Asp 1540	AAA Lys	GTG Val	AAA Lys	Asn	CTT Leu 545	TTT Phe	GAT Asp	GAA Glu	Lys	GAG Glu L550	CAA Gln	GGT Gly	ACT Thr	Ser	GAA Glu 555	4893
ATC . Ile '	ACC . Thr	AGT Ser	Phe	AGC Ser 560	CAT His	CAA Gln	TGG Trp	Ala	AAG Lys 565	ACC Thr	CTA Leu	AAG Lys	Tyr	AGA Arg 570	GAG Glu	4941
GCC :	IGT :	Lys .	GAC Asp 575	CTT Leu	GAA Glu	TTA Leu	Ala	TGT Cys 580	GAG Glu	ACC Thr	ATT Ile	Glu	ATC Ile 585	ACA Thr	GCT Ala	4989

GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn 1590 1595 1600	5037
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn 1605 1610 1615	5085
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu 1620 1635	5133
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro 1640 1645 1650	5181
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser 1655 1660 1665	5229
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln 1670 1675 1680	5277
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp 1685 1690 1695	5325
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu 1700 1715	5373
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His 1720 1725 1730	5421
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn 1735 1740 1745	5469
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu 1750 1760	5517
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val 1765 1770 1775	5565
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys 1780 1785 1790 1795	5613

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu 1800 1805 1810	5661
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT Glu Leu Val Thr Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile 1815 1820 1825	5709
AAA TTG TCC ATA TCT AAT AGT AAT TTT GAG GTA GGG CCA CCT GCA Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala 1830 1835 1840	5757
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile 1845 1850 1855	5805
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys 1860 1865 1870 1875	5853
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala 1880 1885 1890	5901
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser 1895 1900 1905	5949
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp 1910 1915 1920	5997
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu 1925 1930 1935	6045
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser 1940 1945 1950 1955	6093
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser 1960 1965 1970	6141
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln 1975 1980 1985	6189
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile 1990 1995 2000	6237

GA <i>I</i> Glu	A GAT Asp 2005	Ser	ACC Thr	AAG Lys	Gln	GTC Val 2010	TTT Phe	TCC Ser	: AAA : Lys	GTA Val	TTG Leu 2015	TTT Phe	AAA Lys	. AGT Ser	AAC Asn	6285
GAZ Glu 2020	1 His	TCA Ser	GAC Asp	Gln	CTC Leu 2025	ACA Thr	AGA Arg	GAA Glu	Glu	AAT Asn 2030	ACT Thr	GCT Ala	ATA Ile	Arg	ACT Thr 2035	6333
CCA Pro	GAA Glu	CAT His	Leu	ATA Ile 2040	TCC Ser	CAA Gln	AAA Lys	Gly	TTT Phe 2045	TCA Ser	TAT Tyr	AAT Asn	Val	GTA Val 2050	AAT Asn	6381
TCA Ser	TCT Ser	Ala	TTC Phe 2055	TCT Ser	GGA Gly	TTT Phe	Ser	ACA Thr 2060	GCA Ala	AGT Ser	GGA Gly	Lys	CAA Gln 2065	GTT Val	TCC Ser	6429
ATT Ile	Leu	GAA Glu 2070	AGT Ser	TCC Ser	TTA Leu	His	AAA Lys 2075	GTT Val	AAG Lys	GGA Gly	GTG Val	TTA Leu 2080	GAG Glu	GAA Glu	TTT Phe	6477
Asp	TTA Leu 2085	ATC Ile	AGA Arg	ACT Thr	Glu	CAT His 2090	AGT Ser	CTT Leu	CAC His	Tyr	TCA Ser 2095	CCT Pro	ACG Thr	TCT Ser	AGA Arg	6525
CAA Gln 2100	AAT Asn	GTA Val	TCA Ser	Lys	ATA Ile 2105	CTT Leu	CCT Pro	CGT Arg	Val	GAT Asp 2110	AAG Lys	AGA Arg	AAC Asn	Pro	GAG Glu 2115	6573
CAC His	TGT Cys	GTA Val	Asn	TCA Ser 2120	GAA Glu	ATG Met	GAA Glu	Lys	ACC Thr 2125	TGC Cys	AGT Ser	AAA Lys	Glu	TTT Phe	AAA Lys	6621
TTA Leu	TCA Ser	Asn	AAC Asn 2135	TTA Leu	AAT Asn	GTT Val	Glu	GGT Gly 2140	GGT Gly	TCT Ser	TCA Ser	Glu	AAT Asn 2145	AAT Asn	CAC His	6669
TCT Ser	Ile	AAA Lys 2150	GTT Val	TCT Ser	CCA Pro	Tyr	CTC Leu 155	TCT Ser	CAA Gln	TTT Phe	CAA Gln 2	CAA Gln 160	GAC Asp	AAA Lys	CAA Gln	6717
Gln	TTG Leu 2165	GTA Val	TTA Leu	GGA Gly	Thr	AAA Lys 170	GTC Val	TCA Ser	CTT Leu	Val	GAG Glu 175	AAC Asn	ATT Ile	CAT His	GTT Val	6765
TTG Leu 2180	GGA Gly	AAA Lys	GAA Glu	Gln	GCT Ala 185	TCA Ser	CCT Pro	AAA Lys	Asn	GTA Val 190	AAA Lys	ATG Met	GAA Glu	Ile	GGT Gly 195	6813
AAA Lys	ACT Thr	GAA Glu	Thr	TTT Phe 200	TCT Ser	GAT Asp	GTT Val	Pro	GTG Val 205	AAA Lys	ACA Thr	AAT Asn	Ile	GAA Glu 210	GTT Val	6861

TGI Cys	TCI Ser	ACT Thr	TAC Tyr 2215	Ser	: AAA : Lys	GAT Asp	TCA Ser	GAA Glu 2220	. Asn	TAC Tyr	TTT Phe	GAA Glu	ACA Thr 2225	Glu	GCA Ala	6909
GTA Val	GAA Glu	ATT Ile 2230	GCT Ala	AAA Lys	GCT Ala	Phe	ATG Met 2235	Glu	GAT Asp	GAT Asp	GAA	CTG Leu 2240	Thr	GAT Asp	TCT Ser	6957
Lys	CTG Leu 2245	Pro	AGT Ser	CAT His	Ala	ACA Thr 2250	CAT His	TCT Ser	CTT Leu	Phe	ACA Thr 2255	TGT Cys	CCC Pro	GAA Glu	AAT Asn	7005
GAG Glu 2260	Glu	ATG Met	GTT Val	Leu	TCA Ser 2265	AAT Asn	TCA Ser	AGA Arg	Ile	GGA Gly 2270	AAA Lys	AGA Arg	AGA Arg	Gly	GAG Glu 2275	7053
CCC Pro	CTT Leu	ATC Ile	Leu	GTG Val 2280	GGA Gly	GAA Glu	CCC Pro	Ser	ATC Ile 2285	AAA Lys	AGA Arg	AAC Asn	Leu	TTA Leu 2290	AAT Asn	7101
GAA Glu	TTT Phe	Asp	AGG Arg 2295	ATA Ile	ATA Ile	GAA Glu	Asn	CAA Gln 2300	GAA Glu	AAA Lys	TCC Ser	TTA Leu	AAG Lys 2305	GCT Ala	TCA Ser	7149
AAA Lys	Ser	ACT Thr 2310	CCA Pro	GAT Asp	GGC Gly	Thr	ATA Ile 2315	AAA Lys	GAT Asp	CGA Arg	Arg	TTG Leu 2320	TTT Phe	ATG Met	CAT His	7197
His	GTT Val 2325	TCT Ser	TTA Leu	GAG Glu	Pro	ATT Ile 2330	ACC Thr	TGT Cys	GTA Val	Pro	TTT Phe 2335	CGC Arg	ACA Thr	ACT Thr	AAG Lys	7245
GAA Glu 2340	CGT Arg	CAA Gln	GAG Glu	Ile	CAG Gln 345	AAT Asn	CCA Pro	AAT Asn	Phe	ACC Thr 2350	GCA Ala	CCT Pro	GGT Gly	Gln	GAA Glu 2355	7293
TTT Phe	CTG Leu	TCT Ser	Lys	TCT Ser 360	CAT His	TTG Leu	TAT Tyr	Glu	CAT His 365	CTG Leu	ACT Thr	TTG Leu	Glu	AAA Lys 2370	TCT Ser	7341
TCA Ser	AGC Ser	Asn	TTA Leu 375	GCA Ala	GTT Val	TCA Ser	Gly	CAT His	CCA Pro	TTT Phe	TAT Tyr	CAA Gln	GTT Val 2385	TCT Ser	GCT Ala	7389
ACA Thr	Arg	AAT Asn 390	GAA Glu	AAA Lys	ATG Met	Arg	CAC His 395	TTG Leu	ATT Ile	ACT Thr	Thr	GGC Gly 2400	AGA Arg	CCA Pro	ACC Thr	7437
Lys	GTC Val	TTT Phe	GTT Val	CCA Pro	Pro	TTT Phe 410	AAA Lys	ACT Thr	AAA Lys	Ser	CAT His 415	TTT Phe	CAC His	AGA Arg	GTT Val	7485

	Gln		GTT Val	Arg		Ile			Glu		Asn			Lys	CAA Gln 2435	7533
AAC Asn	ATT	GAT Asp	GGA Gly	CAT His 2440	GGC Gly	TCT Ser	GAT Asp	Asp	AGT Ser 2445	AAA Lys	AAT Asn	AAG Lys	Ile	AAT Asn 2450	GAC Asp	7581
		Ile	CAT His 2455				Lys					Gln				7629
	Thr		ACA Thr			Glu					Asp					7677
Leu			GCC Ala		Asp					Arg						7725
			GTC Val	Phe					Ser					Lys		7773
			CCT Pro					Lys					Gly			7821
CCC Pro	TCT Ser	Ala	TGT Cys 2535	TCT Ser	CAT His	AAA Lys	Gln	CTG Leu 2540	TAT Tyr	ACG Thr	TAT Tyr	Gly	GTT Val 2545	TCT Ser	AAA Lys	7869
	Cys		AAA Lys			Ser					Ser					7917
Thr	GAA Glu 2565	GAT Asp	TAT Tyr	TTT Phe	Gly	AAG Lys 2570	GAA Glu	AGT Ser	TTA Leu	Trp	ACT Thr 2575	GGA Gly	AAA Lys	GGA Gly	ATA Ile	7965
CAG Gln 2580	TTG Leu	GCT Ala	GAT Asp	Gly	GGA Gly 585	TGG Trp	CTC Leu	ATA Ile	Pro	TCC Ser	AAT Asn	GAT Asp	GGA Gly	Lys	GCT Ala 595	8013
GGA Gly	AAA Lys	GAA Glu	GAA Glu 2	TTT Phe 600	TAT Tyr	AGG Arg	GCT Ala	Leu	TGT Cys 605	GAC Asp	ACT Thr	CCA Pro	Gly	GTG Val	GAT Asp	8061
CCA Pro	AAG Lys	Leu	ATT Ile 615	TCT Ser	AGA Arg	ATT Ile	Trp	GTT Val 620	TAT Tyr	AAT Asn	CAC His	Tyr	AGA Arg 625	TGG Trp	ATC Ile	8109

	Trp		Leu			Met		Cys			Pro		Glu		GCT Ala	8157
Asn					Pro					Leu	CAA Gln 2655				AGA Arg	8205
				Ile					Arg		GCT Ala			Lys		8253
			Asp					Lys			GTT Val		Cys			8301
		Ile					Asn				ACT Thr	Ser				8349
	Ser					Gln					ATT Ile					8397
Gly	TGG Trp 2725	TAT Tyr	GCT Ala	GTT Val	Lys	GCC Ala 2730	CAG Gln	TTA Leu	GAT Asp	Pro	CCC Pro 2735	CTC Leu	TTA Leu	GCT Ala	GTC Val	8445
TTA Leu 2740	AAG Lys	AAT Asn	GGC Gly	Arg	CTG Leu 2745	ACA Thr	GTT Val	GGT Gly	Gln	AAG Lys 2750	ATT Ile	ATT Ile	CTT Leu	His	GGA Gly 2755	8493
			Val					Ala			CCT Pro		Glu			8541
		Leu					Ser				ACT Thr	Arg				8589
TGG Trp	Tyr	ACC Thr 790	AAA Lys	CTT Leu	GGA Gly	Phe	TTT Phe 795	CCT Pro	GAC Asp	CCT Pro	AGA Arg 2	CCT Pro	TTT Phe	CCT Pro	CTG Leu	8637
Pro					Phe					Asn	GTT Val					8685
GTA Val 2820	ATT Ile	ATT Ile	CAA Gln	Arg	GCA Ala 825	TAC Tyr	CCT Pro	ATA Ile	Gln	TGG Trp 830	ATG Met	GAG Glu	AAG Lys	Thr	TCA Ser	8733

			Tyr					Glu					ГÀв		GCA Ala	8781
		Tyr					Gln					Ala			ACT Thr	8829
	Ile					Glu					Asn	ACA Thr 2880			CCA Pro	8877
Tyr					Ala					Gln		CGT Arg			CAA Gln	8925
				Leu					Lys			GCA Ala		Pro		8973
			Gly					Glu				GCC Ala	Leu			9021
		Gln					Lys					ATC Ile				9069
	Arg					Ser					Glu	CAA Gln 2960				9117
Arg					Val					Ile		AGC Ser				9165
				Ser					Ile			CCA Pro		ser		9213
			Leu					Lys				ATT Ile	Tyr			9261
GCA Ala		Ser					Lys									9309
GCA Ala	Ala					Gln					Pro					9357

			Tyr			CGC Arg		Glu					Lys		GCA Ala	8781
		Tyr				CAA Gln	Gln					Ala		Phe		8829
	Ile					GAA Glu					Asn					8877
Tyr					Ala	CTA Leu 2890				Gln						8925
				Leu		GAA Glu			Lys					Pro		8973
			Gly			AGT Ser		Glu					Leu			9021
		Gln				GAT Asp	Lys					Ile				9069
	Arg					TCT Ser					Glu					9117
Arg					Val	TGG Trp 2970				Ile						9165
				Ser		ATA Ile			Ile					Ser		9213
			Leu			GAA Glu		Lys					Tyr			9261
		Ser				AGT Ser	Lys					Asn				9309
	Ala					CAG Gln 3					Pro					9357

ATT 1					Tyr					Pro					9405
TTT Phe 1				Asp					Cys					Leu	9453
GGA Gly			Val					Lys					Pro		9501
TAT T		Ser					Asn					Lys			9549
GAC (Leu					Ile					Leu				9597
AAC (Asn)					Pro					Gly					9645
GCT (Ala (3140				Ser					Ser					His	9693
CAA (Phe					Asn					Ile		9741
CTT :		Asn					Lys					Leu			9789
GAT (Asp 1	?ro					Pro					Thr				9837
ACT (Thr A					Pro					Lys					9885
CCT A Pro A 3220				Ile					Pro					Met	9933
AAA A Lys A			Ser					Val					Thr		9981

101						GAG										10029
Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn	Cys	Lys	Lys	
			3255					3260					3265	-	-	
AGA	AGA	GCC	ттG	GAT	TTC	TTG	AGT	AGA	СТС	CCT	ጥጥል	CCT	CCA	CCT	CTTT	10077
						Leu										10077
1119		3270	пец	дар	FIIC			Arg	Беп	PIO			PIO	PLO	vaı	
	•	32/0				-	3275				-	3280				
						GTT										10125
Ser	Pro	Ile	Cys	Thr	Phe	Val	Ser	Pro	Ala	Ala	Gln	Lys	Ala	Phe	${ t Gln}$	
3	3285				:	3290					3295					
CCA	CCA	AGG	AGT	TGT	GGC	ACC	AAA	TAC	GAA	ACA	CCC	ATA	AAG	AAA	AAA	10173
						Thr										
3300					3305		2			3310				-	3315	
									•	7510				•	33 I 3	
CDA	СТС	א א ידי	TOT	CCT	CAG	ATG	7 (77)	007	mana	א א א	7. 7. 7.	шша	20 70 000	<i>(</i> 17.7	» mm	10001
																10221
Giu	Leu	ASII			GIII	Met	Thr			гув	гÀв	Pne			IIe	
			2	3320				3	3325					3330		
						TCA										10269
Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu	Ala	Leu	Ile	
		3	3335				3	3340				3	3345			
AAT	ACC	CAA	GCT	CTT	TTG	TCT	GGT	TCA	ACA	GGA	GAA	AAA	CAA	ттт	ΔΤΔ	10317
						Ser										
		3350					355			1		3360		1 110	110	
						_	,,,,,				-	,,,,,,				
ጥርጥ	GTC	ΔСТ	CAA	TCC	አ ርጥ	AGG	7 (717)	CCT	CCC	7.00	7. CITI	max	<i>(</i> 177	C 7 C	m» m	10265
																10365
		Ser	GLU	per		Arg	T 11 T.	Ата	Pro			ser	Gru	Asp	Tyr	
3	365				2	3370				2	3375					
						TGT										10413
Leu	Arg	Leu	Lys	Arg	Arg	Cys	$\operatorname{Th} r$	Thr	Ser	Leu	Ile	Lys	Glu	Gln	Glu	
3380				3	3385				3	390				3	3395	
AGT	TCC	CAG	GCC	AGT	ACG	GAA	GAA	TGT	GAG	AAA	AAT	AAG	CAG	GAC	ACA	10461
Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cvs	Glu	Lvs	Asn	LVS	Gln	Asn	Thr	10101
				400					405	_15				3410	1111	
			~					-	100				-) 1 T O		
מידי ב	מ כי מ	ΔСТ	Z Z Z	7\7\7\	тлт	ATC	יע עניווי									7040=
							TWH									10485
тте	TIIL	Thr		ьys	ryr	тте										
		3	415													

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
 - (A) NAME/KEY: variation
 - (B) LOCATION: 1132
 - (D) OTHER INFORMATION: Xaa = Lys (from codon AAR, R = A or G).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met 1	Pro	Ile	Gly	Ser 5	Lys	Glu	Arg	Pro	Thr 10	Phe	Phe	Glu	Ile	Phe 15	Lys
Thr	Arg	Cys	Asn 20	Lys	Ala	Asp	Leu	Gly 25	Pro	Ile	Ser	Leu	Asn 30	Trp	Phe
Glu	Glu	Leu 35	Ser	Ser	Glu	Ala	Pro 40	Pro	Tyr	Asn	Ser	Glu 45	Pro	Ala	Glu
Glu	Ser 50	Glu	His	Lys	Asn	Asn 55	Asn	Tyr	Glu	Pro	Asn 60	Leu	Phe	Lys	Thr
65					70					75	Ser				80
				85					90		Gln			95	_
			100					105			Asn		110		
		115					120				Met	125			_
	130					135					Ser 140				
Val 145	Leu	Gln	Cys	Thr	His 150	Val	Thr	Pro	Gln	Arg 155	Asp	ГÀЗ	Ser	Val	Val 160
				165					170		Lys			175	
			180					185			Val		190		
		195					200				Leu	205			
	210					215					Val 220				
225					230					235	His	_			240
				245					250		Asp			255	
			260					265		-	Lys		270	_	
		275					280				Gly	285			
	290					295					Val 300				
305					310					315	Arg				320
Gln	Lys	Val	Arg	Thr 325	Ser	Lys	Thr	Arg	Lys 330	Lys	Ile	Phe	His	Glu 335	Ala

Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr 340 345 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser 360 Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu 390 395 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile 405 410 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu 420 425 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg 440 445 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val 455 Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys 470 475 Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser 490 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro 500 505 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn 520 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr 535 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn 550 555 Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn 565 570 Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr 585 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp 600 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala 615 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His 630 635 Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr 650 Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg 660 665 Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr 680 Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro 695 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp 710 715 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala 725 730 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp 745

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Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
                            760
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
                        775
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
                    790
                                         795
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
                                    810
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
            820
                                825
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
                            840
                                                 845
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
                        855
                                            860
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
                    870
                                        875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
                885
                                    890
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
            900
                                905
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
                            920
                                                925
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
                        935
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
                    950
                                        955
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
                965
                                    970
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asp Tyr Met Asn Lys
            980
                                985
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
                            1000
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
                        1015
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
                    1030
                                        1035
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
                1045
                                    1050
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
            1060
                                1065
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
                            1080
                                                1085
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
                        1095
                                            1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
                    1110
                                        1115
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Xaa Pro Ser Tyr Ile
                1125
                                    1130
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
            1140
                                1145
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
        1155
                            1160
                                                1165
```

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Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
                       1175
                                           1180
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
1185
                   1190
                                       1195
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
                1205
                                    1210
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
            1220
                                1225
                                                   1230
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
        1235
                            1240
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
                        1255
                                           1260
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
                    1270
                                      1275
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
                1285
                         1290
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
           1300
                               1305
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
                           1320
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
                        1335
                                           1340
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
                   1350
                                      1355
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
                1365
                                   1370
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
            1380
                               1385
                                                   1390
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
                           1400
                                               1405
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
                       1415
                                           1420
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
                   1430
                                       1435
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
               1445
                                   1450
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
           1460
                              1465
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
                          1480
                                              1485
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
                       1495
                                           1500
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
                   1510
                                      1515
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
               1525
                                   1530
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
           1540
                               1545
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
                           1560
                                               1565
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
                       1575
                                           1580
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Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
                  1590
                                     1595
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
               1605
                                  1610
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
                              1625
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
                          1640
                                             1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
                     1655
                                         1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
                  1670
                                     1675
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
              1685
                                 1690
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
           1700
                  1705
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
    1715
                          1720
                                             1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
                       1735
                                          1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
                  1750
                                     1755
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
               1765
                                 1770
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
           1780
                             1785
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
       1795
                         1800
                                             1805
Cys Val Glu Glu Leu Val Thr Ser Ser Pro Cys Lys Asn Lys Asn
                      1815
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
                   1830
                                      1835
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
               1845
                                  1850
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
           1860
                             1865
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
                          1880
                                             1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
                      1895
                              1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
                  1910
                                      1915
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
               1925
                                  1930
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
           1940
                              1945
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
                          1960
                                             1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
                      1975
                                         1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
                  1990
                                      1995
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Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
               2005
                                   2010
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arq Glu Glu Asn Thr Ala
                               2025
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
                           2040
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
                       2055
                                           2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
                   2070
                                       2075
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
               2085
                                   2090
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
                    2105
            2100
                                                   2110
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
        2115
                          2120
                                              2125
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
                      2135
                                           2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
                   2150
                                       2155
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
                2165
                                   2170
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
           2180
                               2185
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
                          2200
                                               2205
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
                       2215
                                           2220
Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
                   2230
                                       2235
Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
               2245
                                   2250
Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
            2260
                               2265
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
                           2280
                                              2285
Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
                      2295
                                          2300
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
                   2310
                                       2315
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
               2325
                                  2330
Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
           2340
                               2345
Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
                           2360
Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
                       2375
                                           2380
Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
                   2390
                                      2395
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
               2405
                                   2410
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His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
           2420
                               2425
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
                           2440
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
                        2455
                                           2460
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
                    2470
                                       2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
                2485
                                   2490
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
           2500
                              2505
                                                   2510
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
                           2520
                                               2525
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
                       2535
                                           2540
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
                   2550
                                       2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
                2565
                                   2570
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
           2580
                               2585
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
                           2600
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
                       2615
                                           2620
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
                   2630
                                       2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
               2645
                                   2650
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Ser Ala Ile
                               2665
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
                           2680
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
                       2695
                                           2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
                   2710
                                       2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
               2725
                                   2730
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
           2740
                              2745
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
       2755
                           2760
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
                       2775
                                           2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
                   2790
                                       2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
               2805
                                   2810
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
           2820
                               2825
```

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Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
        2835
                           2840
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
                       2855
                                            2860
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
                    2870
                                        2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
                2885
                                    2890
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
            2900
                               2905
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
                           2920
                                               2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
                       2935
                                           2940
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
                   2950
                                       2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
                2965
                                    2970
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
            2980
                                2985
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
        2995
                           3000
                                               3005
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
                       3015
                                           3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
                    3030
                                        3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
                3045
                                   3050
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
            3060
                               3065
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
                           3080
                                               3085
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
                        3095
                                           3100
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
                   3110
                                       3115
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
                                   3130
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
            3140
                               3145
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
       3155
                           3160
                                               3165
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
                       3175
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
                   3190
                                       3195
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
                3205
                                   3210
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
           3220
                               3225
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
                           3240
                                               3245
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Thr			Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn
	3250)				3255	5				3260)			
Cys	Lys	Lys	Arg	Arg	Ala	Leu	Asp	Phe	Leu	Ser	Arg	Leu	Pro	Leu	Pro
3265	5				3270)				3275	5				328
Pro	Pro	Val	Ser	Pro	Ile	Cys	Thr	Phe	Val	Ser	Pro	Ala	Ala	${\tt Gln}$	Lys
				3285	5				3290)				3295	5
Ala	Phe	Gln	Pro	Pro	Arg	Ser	Cys	Gly	Thr	Lys	Tyr	Glu	Thr	Pro	Ile
			3300)				3305	5				3310)	
Lys	Lys	Lys	Glu	Leu	Asn	Ser	Pro	Gln	Met	Thr	Pro	Phe	Lys	Lys	Phe
		3315	5				3320)				3325	5		
Asn	Glu	Ile	Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu
	3330)				3335	5				3340)			
Ala	Leu	Ile	Asn	Thr	Gln	Ala	Leu	Leu	Ser	Gly	Ser	Thr	Gly	Glu	Lys
3345	5				3350)				3355	5				336
Gln	Phe	Ile	Ser	Val	Ser	Glu	Ser	Thr	Arg	Thr	Ala	Pro	Thr	Ser	Ser
				3365	5				3370)				3375	5
Glu	Asp	Tyr	Leu	Arg	Leu	Lys	Arg	Arg	Cys	Thr	Thr	Ser	Leu	Ile	Lys
			3380)				3385	5				3390)	
Glu	Gln	Glu	Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys
		3395	5				3400)				3405	5		
Gln	Asp	Thr	Ile	Thr	Thr	Lys	Lys	Tyr	Ile						
	3410)				3415	5								

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 229...10482
 - (D) OTHER INFORMATION: BRCA2 (OMI3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTGGCGCGA GCTTCTGAAA	CTAGGCGGCA	GAGGCGGAGC	CGCTGTGGCA	CTGCTGCGCC	60
TCTGCTGCGC CTCGGGTGTC	TTTTGCGGCG	GTGGGTCGCC	GCCGGGAGAA	GCGTGAGGGG	120
ACAGATTTGT GACCGGCGCG	GTTTTTGTCA	GCTTACTCCG	GCCAAAAAAG	AACTGCACCT	180
CTGGAGCGGA CTTATTTACC	AAGCATTGGA	GGAATATCGT	AGGTAAAA AT	G CCT ATT	237
			Mε	et Pro Ile	

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC

Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys

5 10 15

		GAT Asp							333
		GCT Ala							381
		AAC Asn 55							429
		TAT Tyr							477
_		ACT Thr							525
		TTA Leu							573
		ACA Thr							621
		CTA Leu 135							669
		GTA Val							717
		ACA Thr							765
		AGT Ser							813
		GCT Ala							861
		GAA Glu 215							909

		TTT Phe						957
		TCT Ser						1005
		GGA Gly 265						1053
		GAC Asp						1101
		GAA Glu						1149
		TCT Ser						1197
		AGG Arg						1245
		AAA Lys 345						1293
		AAT Asn						1341
		GAG Glu						1389
		TGT Cys						1437
		GAG Glu						1485
		GAA Glu 425						1533

		_						TCT Ser 450	1581
								AAT Asn	1629
								CTT Leu	1677
								TTT Phe	1725
								GAG Glu	1773
								AAA Lys 530	1821
								TGC Cys	1869
								AGC Ser	1917
								GGT Gly	1965
								ATA Ile	2013
								AAA Lys 610	2061
								GAA Glu	2109
	_							TCT Ser	2157

			AAT Asn 650					2205
			ATT Ile					2253
			ATC Ile					2301
			CTA Leu					2349
			GAA Glu					2397
			AAA Lys 730					2445
			GTG Val					2493
			GAT Asp					2541
			GTT Val					2589
			ATG Met					2637
			ACC Thr 810					2685
			GAA Glu					2733
			GTA Val					2781

									AAT Asn				2829
									TCT Ser				2877
									GCT Ala 895				2925
									GAA Glu				2973
									ATG Met				3021
									ATT Ile				3069
									GTA Val				3117
									ATC Ile 975				3165
									GAC Asp				3213
			Pro				Ser		GGT Gly		Phe		3261
		Asn				Leu			AAC Asn	Ile			3309
	Met				Ile				CCT Pro				3357
Cys				Asn				Asp	AAT Asn				3405

				Ser					Ser		CAT His			Ser	3453
_			Ser					Ser			ACC Thr		Gln		3501
		Lys					Ser				TTA Leu	Thr			3549
	Ala					Leu					GAA Glu				 3597
Gln					Gln					Ser	TAC Tyr 1135				3645
				Val					Met		ATC Ile			Thr	3693
	_		Cys					Leu			ATA Ile		Asn		3741
		${\tt Gly}$					Ser				GAA Glu	Gly			3789
	Lys					Gly					GAC Asp				3837
Ala					Thr					Val	GGG Gly L215				3885
				Gly					Val		ACT Thr			Leu	3933
			Lys					Ile			ATT Ile		Glu		 3981
		Glu					Ser				AGT Ser	Lys			4029

	Val	GTT Val 1270				Lys					Asn				4077
Ser		AAA Lys			Lys					Leu					4125
		ACT Thr		Thr					Ile					Lys	4173
		GAA Glu	Asn					Tyr					Arg		4221
		TTA Leu					Ser					Asn			4269
	Ile	CAT His 1350				Thr					Thr				4317
Ile		CTT Leu			Ser					Lys					4365
		GAA Glu		Leu					Phe					Lys	4413
		GCA Ala	Cys					Ser					Leu		4461
		ACG Thr					Lys					Ser			 4509
	Gln	ACT Thr L430				Lys					Ala				4557
Asn		ATT Ile			Phe					Pro					4605
		TTA Leu		Ser					Asp					Lys	4653

			Ser		GAG Glu			Asp					Lys		4701
		Ser			GTT Val		Thr					Val			4749
	Gln				GAT 'Asp	Glu					Pro				4797
Phe					GGG Gly					Ile					4845
				Asn	CTT Leu 1545				Lys					Ser	4893
			Phe		CAT His			Ala					Tyr		4941
		Lys			GAA Glu		Ala					Glu			4989
_	Pro				GAA Glu	Met					Asn				5037
Leu					ACT Thr					Lys					5085
				Thr	GAA Glu 1625				Thr					Phe	5133
			۷al		GAA Glu			Glu					Lys		5181
		Cys			AAT Asn		Ser					Ile			5229
	Leu				ACA Thr	Ser					Thr				5277

Thr					GCA Ala					Arg					5325
				Arg	ATA Ile 1705				Asp					Tyr	5373
			Asn		AAC Asn			Ile					Lys		5421
		Glu			GAT Asp		Tyr					Ser			5469
	Tyr				TCT Ser	Asp					Asp				5517
Ser					GAT Asp					Pro					5565
				Asn	ACT Thr 1785				Lys					Val	5613
			Ala		CCA Pro			Val					Cys		5661
		Val			TCT Ser		Pro					Asn			5709
	Leu				AAT Asn	Ser					Val				5757
Phe					GGT Gly					Val					5805
				Asp	ATA Ile 1865				Ser					Ile	5853
			Glu		AAA Lys			Ile					Ile		5901

		TAC Tyr					Asp					Leu			5949
	Asp	AAT Asn 1910				Ser					Lys				5997
Ile		AGT Ser			Ile					Gln			_		 6045
		GTT Val		Lys					Asp	_				Thr	 6093
		TGT Cys	Lys					Lys					Val		6141
		ACT Thr					Ser					Lys			6189
	Ser	GAT Asp 1990	_			Gln					Val				6237
Glu		AGT Ser			Gln					Val					6285
_		TCA Ser		Gln					Glu					Arg	6333
		CAT His	Leu					Gly					Val		6381
		GCT Ala					Ser					Lys			6429
	Leu	GAA Glu 2070				His					Val				6477
Asp		ATC Ile			Glu					Tyr					6525

				Lys					Val		AAG Lys			Pro		6573
			Asn					Lys			AGT Ser		Glu			6621
		Asn					Glu				TCA Ser	Glu				6669
	Ile					Tyr					CAA Gln					6717
Gln					Thr					Val	GAG Glu 2175					6765
	_		_	Gln	_				Asn	_	AAA Lys			Ile	_	6813
			Thr					Pro			ACA Thr		Ile			6861
		Thr					Ser				TTT Phe	Glu				6909
	Glu					Phe					GAA Glu					6957
Lys					Ala					Phe	ACA Thr 2255					7005
			_	Leu					Ile		AAA Lys			Gly		7053
			Leu					Ser			AGA Arg		Leu			7101
		Asp					Asn				TCC Ser	Leu				7149

GC ACT er Thr 2310				Thr					Arg				7197
TT TCT al Ser 25			Pro					Pro					7245
GT CAA rg Gln		Ile					Phe					Gln	7293
rG TCT eu Ser	Lys					Glu					Glu		7341
GC AAT er Asn					Gly					Gln			7389
GA AAT rg Asn 2390				Arg					Thr				7437
TC TTT al Phe 05			Pro					Ser					7485
AG TGT ln Cys		Arg					Glu					Lys	7533
IT GAT le Asp	Gly					Asp					Ile		7581
AG ATT lu Ile					Lys					Gln			 7629
CT TTC ir Phe 2470				Glu					Asp				7677
AG AAT Ln Asn 35			Asp					Arg					7725
AA CGC ln Arg		Phe					Ser					Lys	7773

		CTG Leu	Pro					Lys					Gly		7821
		GCG Ala					Gln					Gly			7869
_	Cys	ATA Ile 2550				Ser					Ser				7917
Thr		GAT Asp			Gly					${\tt Trp}$					7965
		GCT Ala		Gly					Pro					Lys	8013
		GAA Glu	Glu					Leu					Gly		8061
		CTT Leu					${\tt Trp}$					Tyr			8109
	Trp	AAA Lys 2630				Met					Pro				8157
Asn		TGC Cys			Pro					Leu					8205
		ACG Thr		Ile					Arg					Lys	8253
		AGG Arg	Asp					Lys					Cys		8301
		ATT Ile					Asn					Ser			8349
	Ser	AGT Ser 2710				Gln					Ile				8397

	GTT AAG GC Val Lys Al 273	a Gln Leu		ro Leu Leu	8445
	C AGA CTG AC Arg Leu Th 2745				8493
	GGC TCT CC Gly Ser Pr 2760			ro Leu Glu	8541
	TTA AAG AT Leu Lys Il		Asn Ser T		8589
Trp Tyr	CTT GGA TT Leu Gly Ph				8637
	CTT TTC AG Leu Phe Se 281	r Asp Gly		al Gly Cys	8685
	A AGA GCA TA Arg Ala Ty 2825				8733
	C ATA TTT CG Ile Phe Ar 2840			lu Glu Lys	8781
	GAG GCC CA Glu Ala Gl		Arg Leu G		8829
Lys Ile	GAA TTT GA Glu Phe Gl				8877
	CGT GCA CT Arg Ala Le 289	u Thr Arg	Gln Gln V		8925
	CTT TAT GA Leu Tyr Gl 2905				8973
	TAT TTC AG Tyr Phe Se 2920			rg Ala Leu	9021

		CAA Gln					Lys					Ile			9069
	Arg	AAG Lys 2950				Ser					Glu				9117
Arg		GTC Val			Val					Ile					9165
		AAA Lys		Ser					Ile					Ser	9213
		TCT Ser	Leu					Lys					Tyr		9261
		TCA Ser					ГЛЗ					Asn			9309
	Ala	ACA Thr 3030				Gln					Pro				9357
Ile		TTT Phe			Tyr					Pro					9405
		GAT Asp		Asp					Cys					Leu	9453
		GTC Val	Val			-		Lys					Pro		 9501
		TCA Ser					Asn					Lys			9549
	Leu	AAT Asn 3110				Ile					Leu				9597
Asn		CAG Gln			Pro					Gly					9645

			TTT Phe	Ser					Ser					His	9693
			TTC Phe					Asn					Ile		 9741
		Asn	GAA Glu 3175				Lys					Leu			9789
	Pro		TGG Trp			Pro					Thr				9837
Thr			ATC Ile		Pro					Lys					9885
			GAG Glu	Ile					Pro					Met	9933
			TCT Ser					Val					Thr		9981
		Lys	GGG Gly 255				Ile					Asn			10029
	Arg		TTG Leu			Leu					Leu				10077
Ser			TGT Cys		Phe					Ala					10125
			AGT Ser	Cys					Glu					Lys	10173
			TCT Ser					Pro					Asn		10221
		Leu	GAA Glu 335				Ile					Leu			10269

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile 3350 3355 TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Glu Glu 3380 3385 3390 AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3405 ATT ACA ACT AAA AAA TAT ATC TAA 10485 Ile Thr Thr Lys Lys Tyr Ile

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid

3415

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys 1.0 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe 25 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu 40 Glu Ser Glu His Lys Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr 55 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile 70 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys 85 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser 100 105 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp 120 125 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val 135 140

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Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
                    150
                                         155
Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
                165
                                     170
Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
                                185
Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
                            200
                                                 205
Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
                        215
                                             220
Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
                    230
                                         235
Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
                245
                                    250
Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
            260
                                265
Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
                            280
His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
                        295
Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
                    310
                                         315
Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
                                    330
Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
            340
                                345
Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
                            360
                                                 365
Asn Val Ala Asn Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
                        375
Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
                    390
                                         395
Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
                                    410
Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
            420
                                425
Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
                            440
                                                 445
Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
                        455
Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
                    470
                                        475
Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
                                    490
                485
Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
            500
                                505
Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
                            520
Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
                        535
                                            540
Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
                    550
                                        555
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Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
                                    570
                565
Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
                                585
Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
                            600
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
                        615
                                             620
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
                    630
                                        635
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
                645
                                    650
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
                                665
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
                            680
                                                685
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
                        695
                                            700
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
                    710
                                        715
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
                725
                                    730
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
            740
                                745
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
                            760
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
                        775
                                            780
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
                    790
                                        795
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
                                    810
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
                                825
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
                            840
                                                845
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
                        855
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
                    870
                                        875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
                                    890
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
           900
                                905
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
                            920
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
                        935
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
                    950
                                        955
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
                965
                                    970
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Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys
           980
                               985
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
                           1000
                                               1005
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
                       1015
                                           1020
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
                   1030
                                       1035
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
               1045
                                   1050
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
           1060
                               1065
Gln Ser Ser Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
       1075
                           1080
                                              1085
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
                      1095
                                          1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
                   1110
                                       1115
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
                                   1130
                1125
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
           1140
                              1145
                                                   1150
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
                           1160
                                              1165
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
                       1175
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
                   1190
                                       1195
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
               1205
                                   1210
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
            1220
                               1225
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
                           1240
                                               1245
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Lys
                       1255
                                           1260
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
                   1270
                                       1275
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
               1285
                                  1290
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
           1300
                               1305
                                                   1310
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
                           1320
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
                       1335
                                           1340
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
                   1350
                                       1355
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
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                                   1370
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
                               1385
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Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
       1395
                          1400
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
                       1415
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Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
                   1430
                                       1435
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
               1445
                                   1450
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
           1460
                              1465
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
                1480
                                              1485
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
                      1495
                                          1500
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
                  1510
                                      1515
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
               1525
                                   1530
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
            1540
                               1545
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
       1555
                           1560
                                              1565
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
                      1575
                                         1580
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
                   1590
                                      1595
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
               1605
                                  1610
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
           1620
                              1625
                                                  1630
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
                           1640
                                              1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
                       1655
                                          1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
                   1670
                                      1675
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
               1685
                                  1690
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
           1700
                              1705
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
       1715
                          1720
                                              1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
                      1735
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
                   1750
                                      1755
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
                                   1770
               1765
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
                   1785
           1780
                                                  1790
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
                           1800
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Cys Val Glu Glu Leu Val Thr Ser Ser Pro Cys Lys Asn Lys Asn
            1815
                                          1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
                   1830
                                       1835
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
               1845
                                   1850
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
            1860
                               1865
                                                   1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
                           1880
                                              1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
                       1895
                                          1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
                   1910
                                       1915
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
               1925
                                   1930
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
           1940
                               1945
                                                   1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
                           1960
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
   1970
                       1975
                                           1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
                   1990
                                       1995
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
               2005
                                   2010
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
           2020
                               2025
                                                   2030
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
       2035
                           2040
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
                       2055
                                           2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
                   2070
                                       2075
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
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                                   2090
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
                              2105
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
                          2120
                                               2125
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
                      2135
                                           2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
                   2150
                                      2155
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
               2165
                                   2170
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
                               2185
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
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Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
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Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
                   2230
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Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
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Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
            2260
                                2265
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
                           2280
                                               2285
Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
                       2295
                                           2300
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
                   2310
                                       2315
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arq
               2325
                                   2330
                                                       2335
Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
           2340
                               2345
                                                   2350
Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
                           2360
                                               2365
Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
                       2375
Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
                   2390
                                      2395
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
               2405
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His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
            2420
                               2425
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
                           2440
                                               2445
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
                       2455
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Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Pro Leu Asp Leu
                   2470
                                       2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
                2485
                                   2490
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
           2500
                               2505
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
                           2520
                                               2525
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
                       2535
                                           2540
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
                   2550
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Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
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                                   2570
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
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                               2585
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
                           2600
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Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
                       2615
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Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
                   2630
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Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
               2645
                                  2650
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Ser Ala Ile
            2660
                               2665
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
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Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
                        2695
                                           2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
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Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
               2725
                                   2730
                                                       2735
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
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Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
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Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
                       2775
                                           2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
                   2790
                                       2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
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Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
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                              2825
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu
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Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
                       2855
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Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
                   2870
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Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
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                                   2890
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
           2900
                               2905
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
                           2920
                                               2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
                       2935
                                           2940
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
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                                       2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
               2965
                                   2970
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
           2980
                               2985
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
                           3000
                                               3005
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
                       3015
                                           3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
                   3030
                                       3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
                                   3050
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Phe	Ser	Lys	Phe 3060		Asp	Pro	Asp	Phe 306!		Pro	Ser	Сув	Ser 3070		Val
Λαn	T. Ou	т1о			1707	37-1	C			T	T ~	ml			7 J
Asp	пец	Ile 3079		Pile	vai	vai	3080		vaı	гув	гуѕ	3085		ьeu	Ата
Pro	Phe	Val	Tyr	Leu	Ser	Asp	Glu	Cys	Tyr	Asn	Leu	Leu	Ala	Ile	Lys
	3090)				309	5	-			3100)			_
Phe	${\tt Trp}$	Ile	Asp	Leu	Asn	Glu	Asp	Ile	Ile	Lys	Pro	His	Met	Leu	Ile
3105	5				3110)				3115	5				312
Ala	Ala	Ser	Asn	Leu 3125		Trp	Arg	Pro	Glu 3130		Lys	Ser	Gly	Leu 3135	
Th w	T 011	Phe	7.7.			Dho	C 0	T7- 7			7.7 _	G	D		
1111	шец	FIIC			Asp	FIIC	261			ser	AIA	ser		-	GIU
~ 1	TT .	T-1	3140				_	3145		_	_		3150		
GIY	HIS	Phe		GIU	Thr	Pne			Met	гЛг	Asn			Glu	Asn
		3155					3160					3165			
Ile	Asp	Ile	Leu	Cys	Asn	Glu	Ala	Glu	Asn	Lys	Leu	Met	His	Ile	Leu
	3170					3175					3180				
His	Ala	Asn	Asp	Pro	Lys	Trp	Ser	Thr	Pro	Thr	Lys	Asp	Cys	Thr	Ser
3185					3190					3195		-	-		320
Glv	Pro	Tyr	Thr	Ala	Gln	Tle	Tle	Pro	Glv			Δsn	Lvs	T.em	
- 1		-1-		3205				110	3210		CLY	2-10-11		3215	
Mot	Cor	Cor	Dro			G 1	77.	m			Q	Desa			
Mec	ser	Ser			Сув	GIU	тте			GIN	ser	Pro			ьeu
_			3220				_	3225			_		3230		
Cys	Met	Ala		Arg	Lys	Ser			Thr	Pro	Val			Gln	Met
		3235					3240					3245			
Thr	Ser	Lys	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn
	3250)				3255	5				3260)			
Cys	Lys	Lys	Arg	Arg	Ala	Leu	Asp	Phe	Leu	Ser	Arg	Leu	Pro	Leu	Pro
3265		_			3270		-			3275					328
		Val	Ser	Pro			Thr	Phe	Val			Δla	Δla	Gln	
				3285		0,70			3290			1114		3295	_
7.7 -	Dhe	Gln	Dro			Con	Crra	01			TT	<i>α</i> 1			
ніа	PIIC	Gln			ALG	ser	Сув			гуя	TAL	GIU			тте
-	~	-	3300		_	_	_	3305			_		3310		
гàг	гуя	Lys		Leu	Asn				Met	Thr	Pro			Lys	Phe
		3315					3320					3325			
Asn	Glu	Ile	Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu
	3330)				3335	5				3340)			
Ala	Leu	Ile	Asn	Thr	Gln	Ala	Leu	Leu	Ser	Glv	Ser	Thr	Glv	Glu	Lvs
3345					3350					3355			1		336
		Ile	Ser	Va 1			Ser	Thr	Ara			Dro	Thr	Sar	
0111	1110		DCI	3365		Giu	Der	T.11.T.	3370		AIA	PIO			
a1	7		T			T	70				1	_		3375	
GIU	Asp	Tyr			ьeu	ьys				Thr	Thr	Ser			ГЛS
			3380					3385					3390		
Glu	Gln	Glu		Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys
		3395	;				3400)				3405			
Gln	Asp	Thr	Ile	Thr	Thr	Lys	Lys	Tyr	Ile						
	3410					3415	-	-							

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10485 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 229...10482
 - (D) OTHER INFORMATION: BRCA2 (OMI4)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCTGCTGCGC CTC	GGGTGTC TTTTG	CGGCG GTGGGTCGCC	CGCTGTGGCA CTGCTGCGCC GCCGGGAGAA GCGTGAGGGG GCCAAAAAAG AACTGCACCT	60 120 180
			AGGTAAAA ATG CCT ATT Met Pro Ile 1	237
			TTT AAG ACA CGC TGC Phe Lys Thr Arg Cys 15	285
			TGG TTT GAA GAA CTT Trp Phe Glu Glu Leu 35	333
			GCA GAA GAA TCT GAA Ala Glu Glu Ser Glu 50	381
			AAA ACT CCA CAA AGG Lys Thr Pro Gln Arg 65	429
			ATA ATA TTC AAA GAG Ile Ile Phe Lys Glu 80	477
			GTA AAA GAA TTA GAT Val Lys Glu Leu Asp 95	525
			AAT AGT AGA CAT AAA Asn Ser Arg His Lys 115	573
			GCA GAT GAT GTT TCC Ala Asp Asp Val Ser 130	621

				TGT Cys		Glu				669
				CAA Gln						717
				TTT Phe 170						765
				GCT Ala						813
		_	_	CCC Pro						861
				GAA Glu						909
				TCC Ser						957
				GTG Val 250						1005
				TTT Phe						1053
_				CAC His						1101
				ACA Thr						1149
				AAA Lys						1197
				AAA Lys 330						1245

_			AAC Asn						1293
			GAT Asp						1341
_			AGT Ser						1389
			GAA Glu						1437
			AAA Lys 410					-	1485
			AAA Lys						1533
			TCA Ser						1581
			CCA Pro						1629
			CTT Leu						1677
			GGA Gly 490						1725
			TTC Phe						1773
			GGT Gly						1821
			AGT Ser						1869

AAG Lys								1917
GCC Ala 565								1965
TCC Ser						_		2013
GAA Glu								2061
CTA Leu								2109
CTT Leu								2157
AGA Arg 645								2205
AGC Ser								2253
TCT Ser								2301
TGT Cys								2349
CTG Leu								2397
AAA Lys 725								2445
GTA Val								2493

						CTT Leu		2541
						ATT Ile 785		2589
						AAC Asn		2637
						AAG Lys		2685
_						CTG Leu		2733
-						GTA Val		2781
						GAA Glu 865		2829
						GAA Glu		2877
						GAA Glu		2925
						GAC Asp		2973
						TTA Leu		3021
						AAA Lys 945		3069
						CAG Gln		3117

			CTA Leu												3165
			CCA Pro												3213
			CCA Pro					Ser					Phe		3261
		Asn	AAG Lys 1015				Leu					Ile			3309
	Met		TTC Phe			Ile					Pro				3357
Cys			ATT Ile		Asn					Asp					3405
			CAG Gln	Ser					Ser					Ser	3453
			TCT Ser					Ser					Gln		3501
		Lys	CAG Gln L095				Ser					Thr			3549
	Ala		ATT Ile			Leu					Glu				3597
Gln			TTT Phe		Gln					Ser					3645
			GAA Glu	Val					Met					Thr	3693
			TGC Cys 1					Leu					Asn		3741

		Gly					Ser	AAG Lys 1180				Gly			3789
	Lys					Gly		TTG Leu			Asp				3837
Ala					Thr			AAT Asn		Val					3885
				Gly				AAT Asn	Val					Leu	3933
			Lys					ATT Ile					Glu		3981
		Glu					Ser	TTA Leu 1260				Lys			4029
	Val					Lys		GAA Glu			Asn				4077
Ser					Lys			CTG Leu		Leu					4125
				Thr				GAA Glu	Ile					Lys	4173
			Asn					TAT Tyr					Arg		4221
		Leu					ser	GAT Asp 1340				Asn			4269
	Ile					Thr		TTG Leu			Thr				4317
Ile					Ser			TTT Phe		Lys					4365

			GAT Asp	Leu					Phe					rys	4413
			TGT Cys					Ser					Leu		4461
		Thr	GAG Glu 1415				Lys					ser			4509
	Gln		GCA Ala			ГХг					Ala				4557
Asn			GTA Val		Phe					Pro					4605
			AAT Asn	Ser					Asp					Lys	4653
			AGT Ser					Asp					Lys		4701
		Ser	GTC Val 1495				Thr					Val			4749
	Gln		GAA Glu			Glu					Pro				4797
Phe			GCT Ala		Gly					Ile					4845
			AAA Lys	Asn					Lys					Ser	4893
			TTT Phe					Ala					Tyr		4941
		Lys	GAC Asp 1575				Ala					Glu			4989

	Pro				GAA Glu	Met					Asn				5037
Leu					ACT Thr					ГЛЗ					 5085
				Thr	GAA Glu 1625				Thr					Phe	5133
			Val		GAA Glu			Glu					Lys		 5181
		Cys			AAT Asn		Ser					Ile			5229
	Leu				ACA Thr	Ser					Thr				5277
Thr					GCA Ala					Arg					5325
				Arg	ATA Ile 1705				Asp					Tyr	5373
			Asn		AAC Asn			Ile					Lys		5421
		Glu			GAT Asp		Tyr					Ser			5469
	Tyr				TCT Ser	Asp					Asp				5517
Ser					GAT Asp					Pro					5565
_				Asn	ACT Thr 1785				Lys					Val	 5613

			Ala					Val		_	GAT Asp		Cys		5661
		Val					Pro				AAA Lys	Asn			5709
	Leu					Ser				_	GTA Val				 5757
Phe					Gly					Val	TCA Ser 1855				 5805
				Asp					Ser		AGT Ser			Ile	5853
			Glu					Ile			ACG Thr		Ile		5901
		Tyr					Asp				ATT Ile	Leu			5949
	Asp					Ser					AAG Lys				5997
Ile					Ile					Gln	AAT Asn 1935				6045
				Lys					Asp		AGT Ser			Thr	6093
			Lys					Lys			AAG Lys		Val		6141
		Thr					Ser				GGA Gly	Lys			6189
	Ser					Gln					GTG Val				6237

Glu		AGT Ser			Gln					Val					6285
		TCA Ser		Gln					Glu					Arg	6333
		CAT His	Leu					Gly					Val		 6381
		GCT Ala					Ser					ГЛЗ			6429
	Leu	GAA Glu 2070				His					Val				6477
Asp		ATC Ile			Glu					Tyr					6525
		GTA Val		Lys					Val					Pro	6573
		GTA Val	Asn					Lys					Glu		6621
		AAT Asn					Glu					Glu			6669
	Ile	AAA Lys 2150				Tyr					Gln				6717
Gln		GTA Val			Thr					Val					6765
		AAA Lys		Gln					Asn					Ile	6813
		GAA Glu	Thr					Pro					Ile		6861

		ACT Thr					Ser					Glu			6909
	Glu	ATT Ile 2230				Phe					Glu				6957
Lys		CCA Pro			Ala					Phe					7005
		ATG Met		Leu					Ile					Gly	7053
		ATC Ile	Leu					Ser					Leu		7101
		GAC Asp					Asn					Leu			7149
	Ser	ACT Thr 2310				Thr					Arg				7197
His		TCT Ser			Pro					Pro					7245
		CAA Gln		Ile					Phe					Gln	7293
		TCT Ser	Lys					Glu					Glu		7341
		AAT Asn					Gly					Gln			7389
	Arg	AAT Asn 2390				Arg					Thr				7437
Lys		TTT Phe			Pro					ser					74.85

	CAG Gln			Arg					Glu					Lys	7533
	ATT Ile		Gly					Asp					Ile		7581
	GAG Glu	Ile					Lys					Gln			7629
	ACT Thr					Glu					Asp				7677
Leu	CAG Gln 2485				Asp					Arg					7725
	CAA Gln			Phe					Ser					Lys	7773
	ACT Thr		Pro					Lys					Gly		7821
	TCT Ser	Ala					Gln					Gly			7869
	TGC Cys					Ser					Ser				7917
Thr	GAA Glu 2565				Gly					Trp					7965
	TTG Leu			Gly					Pro					ГХв	8013
	AAA Lys		Glu					Leu					Gly		8061
	AAG Lys	Leu				_	Trp					Tyr			8109

	Trp	AAA Lys 2630				Met					Pro				8157
Asn		TGC Cys			Pro					Leu					8205
		ACG Thr		Ile					Arg					Lys	8253
		AGG Arg	Asp					Lys					Cys		8301
		ATT Ile					Asn					Ser			8349
	Ser	AGT Ser 2710				Gln					Ile				8397
Gly		TAT Tyr	-		Lys					Pro					8445
		AAT Asn		Arg					Gln					His	8493
		CTG Leu	Val					Ala					Glu		8541
		CTT Leu					Ser					Arg			8589
	Tyr	ACC Thr 2790				Phe					Arg				8637
Pro		TCA Ser			Phe					Asn					8685
		ATT Ile		Arg					Gln					Thr	8733

			TAC Tyr					Glu					Lys		8781
		Tyr	GTG Val 2855				Gln					Ala			8829
	Ile		GAG Glu			Glu					Asn				8877
Tyr			TCA Ser		Ala					Gln					8925
			GAG Glu	Leu					Lys					Pro	8973
			GGT Gly					Glu					Leu		9021
		Gln	ATG Met 2935				Lys					Ile			9069
	Arg		GCC Ala			Ser					Glu				9117
Arg			ACA Thr		Val					Ile					9165
			GAT Asp	Ser					Ile					Ser	9213
			CTG Leu					Lys					Tyr		9261
		Ser	AAA Lys 3015				Lys					Asn			9309
	Ala		AAA Lys			Gln					Pro				9357

Ile	TTA Leu 3045				Tyr					Pro						9405
_	TTA Leu			Asp					Cys					Leu		9453
	TTT Phe		Val					Lys					Pro			9501
	TTG Leu	Ser					Asn					Lys				9549
	CTT Leu					Ile					Leu				-	9597
Asn	CTC Leu 3125				Pro					Gly						9645
	GGA Gly			Ser					Ser					His		9693
	GAG Glu		Phe					Asn					Ile			9741
	TGC Cys	Asn					Lys					Leu				9789
	CCC Pro					Pro					Thr					9837
Thr	GCT Ala 3205				Pro					Lys						9885
	AAT Asn			Ile					Pro					Met		9933
	AGG Arg		Ser					Val					Thr			9981

		AAA Lys														10029
DCI	СуБ	_	3255	Giù	пур	GIU		3260	nsp	OIII	цуъ		3265	пур	цуз	
AGA	AGA	GCC	TTG	GAT	TTC	TTG	AGT	AGA	CTG	CCT	TTA	CCT	CCA	CCT	GTT	10077
Arg	_	Ala	Leu	Asp	Phe			Arg	Leu	Pro			Pro	Pro	Val	
		3270				3	3275				3	3280				
		ATT														10125
		Ile	Cys	Thr			Ser	Pro	Ala			Lys	Ala	Phe	GIn	
٤	3285				2	3290				-	3295					
		AGG														10173
	Pro	Arg	Ser	-	-	Thr	Lys	Tyr			Pro	Ile	ГЛЗ	_	_	
3300				3	3305				3	3310				3	3315	
GAA	CTG	AAT	TCT	CCT	CAG	ATG	ACT	CCA	TTT	AAA	AAA	TTC	AAT	GAA	ATT	10221
Glu	Leu	Asn			Gln	Met	Thr			Га	ГЛЗ	Phe			Ile	
			3	3320				3	3325				3	3330		
TCT	CTT	TTG	GAA	AGT	AAT	TCA	ATA	GCT	GAC	GAA	GAA	CTT	GCA	TTG	ATA	10269
Ser	Leu	Leu		Ser	Asn	Ser			Asp	Glu	Glu	Leu	Ala	Leu	Ile	
		3	3335				3	3340				:	3345			
AAT	ACC	CAA	GCT	CTT	TTG	TCT	GGT	TCA	ACA	GGA	GAA	AAA	CAA	TTT	ATA	10317
Asn	Thr	Gln	Ala	Leu	Leu	Ser	Gly	Ser	Thr	Gly	Glu	Lys	Gln	Phe	Ile	
	;	3350				:	3355				3	3360				
TCT	GTC	AGT	GAA	TCC	ACT	AGG	ACT	GCT	CCC	ACC	AGT	TCA	GAA	GAT	TAT	10365
		Ser	Glu	Ser		_	Thr	Ala	Pro			Ser	Glu	Asp	Tyr	
:	3365				:	3370					3375					
CTC	AGA	CTG	AAA	CGA	CGT	TGT	ACT	ACA	TCT	CTG	ATC	AAA	GAA	CAG	GAG	10413
Leu	Arg	Leu	Lys	Arg	Arg	Cys	Thr	Thr	Ser	Leu	Ile	Lys	Glu	Gln	Glu	
3380				3	3385				:	3390				3	3395	
AGT	TCC	CAG	GCC	AGT	ACG	GAA	GAA	TGT	GAG	AAA	AAT	AAG	CAG	GAC	ACA	10461
Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys	Gln	Asp	Thr	
			3	3400				3	3405				3	3410		
ATT	ACA	ACT	AAA	AAA	TAT	ATC	TAA					•				10485
		Thr														
		3	3415													

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu His Lys Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile 70 75 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys 90 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser 105 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp 120 125 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val 135 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val 150 155 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr 170 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met 180 185 Ser Trp Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val 200 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp 215 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu 230 235 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr 250 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn 265 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro 280 Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu 295 300 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu 310 315 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala 330 Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr 345 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser 360 Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser

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375
                                             380
Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
                    390
Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
                405
                                    410
Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
                            440
Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
                        455
Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
                    470
                                        475
Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
                485
                                    490
Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
            500
                                505
Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
                            520
Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
                                             540
Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
                    550
                                        555
Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
                565
                                    570
Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
            580
                                585
Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
                            600
                                                605
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
                        615
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
                    630
                                        635
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
                                    650
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
                                665
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
                            680
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
                        695
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
                    710
                                        715
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
               725
                                    730
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
                                745
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
                            760
                                                765
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
                        775
                                            780
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
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790
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
                                     810
 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
             820
                                 825
 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
                             840
 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
                     870
                                         875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
                                     890
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
            900
                                 905
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
                             920
                                                 925
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
                        935
                                             940
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
                    950
                                         955
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
                                     970
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
                                985
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
                            1000
                                                 1005
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
                        1015
                                            1020
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
                    1030
                                        1035
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
                1045
                                    1050
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
            1060
                                1065
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
                            1080
                                                1085
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
                        1095
                                            1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
                    1110
                                        1115
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
                1125
                                    1130
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
            1140
                                1145
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
        1155
                            1160
                                                1165
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
                        1175
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
                    1190
                                        1195
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
```

Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Lys Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser

Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys 1,980 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn

Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln

Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Ser Ala Ile Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr

Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys

22.05	
3285	3290 3295
Ala Phe Gln Pro Pro Arg Ser Cys Gly 3300 3305	3310
Lys Lys Glu Leu Asn Ser Pro Gln 3315 3320	Met Thr Pro Phe Lys Lys Phe
Asn Glu Ile Ser Leu Leu Glu Ser Asn 3330 3335	3325 Ser Ile Ala Asp Glu Glu Leu
Ala Leu Ile Asn Thr Gln Ala Leu Leu	3340
3345 3350	22
Gln Phe Ile Ser Val Ser Glu Ser Thr	3355 336 Arg Thr Ala Pro Thr Ser Ser
3365	3370
Glu Asp Tyr Leu Arg Leu Lys Arg Arg 3380 3385	Cys Thr Thr Ser Leu Ile Lys
Glu Gln Glu Ser Ser Gln Ala Ser Thr	Glu Glu Cvs Glu Twa Aan Twa
3395 3400	3405
Gln Asp Thr Ile Thr Thr Lys Lys Tyr : 3410 3415	Tle
(2) INFORMATION FOR SEQ ID 1	TO 10
(-) IIII SMAILTION FOR BEQ ID I	0:12:
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 10485 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	·
(ix) FEATURE:	
() 1 11101111.	
(A) NAME/KEY: Coding Sequence	<u> </u>
(B) LOCATION: 22910482	-
(D) OTHER INFORMATION: BRCA2	(OMI5)
(1)	
(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:12:
CCTCCCCCA CCTTCTCA A A CTTCCA	
GGTGGCGCA GCTTCTGAAA CTAGGCGGCA GAGG	CGGAGC CGCTGTGGCA CTGCTGCGCC 60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGG	GTCGCC GCCGGGAGAA GCGTGAGGGG 120
ACAGATTTGT GACCGCGCG GTTTTTGTCA GCTT	ACTCCG GCCAAAAAAG AACTGCACCT 180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAA	
	Met Pro Ile
	1
GGA TCC AAA GAG AGG CCA ACA TTT TTT GA	A ATT TTT AAG ACA CCC TCC
Gly Ser Lys Glu Arg Pro Thr Phe Phe Gl	u Ile Phe Lys Thr Arg Cys
5 10	15
AAC AAA GGA GAT	
AAC AAA GCA GAT TTA GGA CCA ATA AGT CT	T AAT TGG TTT GAA GAA CTT 333
on mys ara asp hen Gry Pro The Ser Le	u Asn Trp Phe Glu Glu Leu
25	30 35

TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA 381

Se	r Se	r Gl	u Al	a Pr 40	o Pr	о Ту	r As:	n Sei	r Gli 45	u Pr	o Al	a Gl	u Gl	u Se 50	r Glu	
CA Hi	T AA s Ly	A AA s As	C AA n As 55	n As	T TA n Ty	C GA r Gl	A CC	A AAC ASI 60	C CT	A TT u Ph	T AA e Ly	A AC	T CC. r Pro 65	A CA	A AGG n Arg	42
AA: Ly:	A CC	A TC Se 70	r Ty	T AA' r Asi	T CAG	G CTO	G GC: 1 Ala 75	T TCA a Ser	A ACT	r cc	A AT	A AT e Il 80	A TTO	C AAZ e Lys	A GAG 3 Glu	47
CAA Gli	A GG(n Gl ₃ 85	G CT	G AC	r CTO	G CCC	G CTO Let 90	G TAC	C CAA	TC7	CC'	r GT o Vai	A AA l Lys	A GAZ E Gli	A TTA I Lei	A GAT ı Asp	52!
AAZ Lys 100	Pne	C AA	A TTA	A GAC 1 Asp	TTZ Leu 105	ı Gly	A AGG	AAT Asn	' GTT Val	CCC Pro	Ası	r AG n Sen	T AGA	A CAT	AAA Lys 115	573
AGT Ser	CTI	CGC Arg	C ACA	A GTG Val 120	. Lys	ACT Thr	' AAA ' Lys	ATG Met	GAT Asp 125	Glr	A GCA n Ala	A GAT Asp	GAT Asp	GTT Val	TCC Ser	621
TGT Cys	CCA Pro	CTT Let	CTA Leu 135	ı Asn	TCT Ser	' TGT Cys	CTT Leu	AGT Ser 140	GAA Glu	AGT Ser	CCI Pro	GTI Val	GTT Val	Leu	. CAA Gln	669
TGT Cys	ACA Thr	CAT His	Val	ACA Thr	CCA Pro	CAA Gln	AGA Arg 155	GAT Asp	AAG Lys	TCA Ser	. GTG Val	GTA Val 160	Cys	GGG	AGT Ser	717
TTG Leu	TTT Phe 165	CAT His	' ACA Thr	CCA Pro	AAG Lys	TTT Phe 170	GTG Val	AAG Lys	GGT Gly	CGT Arg	CAG Gln 175	ACA Thr	CCA Pro	AAA Lys	CAT His	765
ATT Ile 180	TCT Ser	GAA Glu	AGT Ser	CTA Leu	GGA Gly 185	GCT Ala	GAG Glu	GTG Val	GAT Asp	CCT Pro 190	GAT Asp	ATG Met	TCT Ser	TGG Trp	TCA Ser 195	813
AGT Ser	TCT Ser	TTA Leu	GCT Ala	ACA Thr 200	CCA Pro	CCC Pro	ACC Thr	CTT Leu	AGT Ser 205	TCT Ser	ACT Thr	GTG Val	CTC Leu	ATA Ile 210	GTC Val	861
AGA Arg	AAT Asn	GAA Glu	GAA Glu 215	GCA Ala	TCT Ser	GAA Glu	ACT Thr	GTA Val 220	TTT Phe	CCT Pro	CAT His	GAT Asp	ACT Thr 225	ACT Thr	GCT Ala	909
AAT Asn	val	AAA Lys 230	AGC Ser	TAT Tyr	TTT Phe	TCC Ser	AAT Asn 235	CAT His	GAT Asp	GAA Glu	AGT Ser	CTG Leu 240	AAG Lys	AAA Lys	AAT Asn	957
GAT	AGA	TTT	ATC	GCT	TCT	GTG	ACA	GAC :	AGT	GAA	AAC	ACA	ААТ	ሮልኔ	ΔGΔ	1005

As	p Ar 24	g Ph 5	e Il	e Al	a Se	r Va 25	l Th O	r As	p Se	r Gl	u Ası 25:		r As	n Gl	n Arg	
GA2 Gl: 260	ı AI	T GC a Al	A AG a Se	T CA r Hi	T GG s Gl; 26	y Ph	T GG e Gl	A AA y Ly:	A AC	A TC	r Gly	G AA Y As:	T TC n Se	A TT r Ph	T AAA e Lys 275	1053
GT <i>I</i> Va]	A AA' L Ası	T AG n Se	C TG r Cy	C AA s Ly: 28	s Ası	C CA	C AT	r GGA	A AAC / Lys 285	s Sei	A ATO	G CC	A CA'	T GT s Vai	C CTA l Leu)	1101
GAA Glu	A GAT 1 Asp	r GA	A GTZ 1 Val 295	T TY	F GAA	A AC	A GT	r GTZ l Val 300	. Asp	ACO Thi	C TCT	GAZ Gli	A GA 1 Gl 305	ı Asr	r AGT Ser	1149
TTT Phe	TCA Ser	1 TTA Let 310	ı Cys	TTT Phe	TCT Ser	AAZ Lys	A TGT Cys 315	: Arg	ACA Thr	. Lys	AAT Asn	CTA Leu 320	ı Glr	A AAZ 1 Lys	A GTA S Val	1197
AGA Arg	ACT Thr 325	Ser	AAC Lys	F ACT	AGG Arg	AAA Lys 330	Lys:	ATT	TTC Phe	CAT His	GAA Glu 335	Ala	AAC Asr	C GCT Ala	GAT Asp	1245
GAA Glu 340	TGT Cys	GAA Glu	AAA Lys	TCT Ser	AAA Lys 345	AAC Asn	CAA Gln	GTG Val	AAA Lys	GAA Glu 350	AAA Lys	TAC Tyr	TCA Ser	TTT Phe	GTA Val 355	1293
TCT Ser	GAA Glu	GTG Val	GAA Glu	CCA Pro 360	AAT Asn	GAT Asp	ACT Thr	GAT Asp	CCA Pro 365	TTA Leu	GAT Asp	TCA Ser	AAT Asn	GTA Val 370	GCA Ala	1341
CAT His	CAG Gln	AAG Lys	CCC Pro 375	TTT Phe	GAG Glu	AGT Ser	GGA Gly	AGT Ser 380	GAC Asp	AAA Lys	ATC Ile	TCC Ser	AAG Lys 385	GAA Glu	GTT Val	1389
GTA Val	CCG Pro	TCT Ser 390	TTG Leu	GCC Ala	TGT Cys	GAA Glu	TGG Trp 395	TCT Ser	CAA Gln	CTA Leu	ACC Thr	CTT Leu 400	TCA Ser	GGT Gly	CTA Leu	1437
AAT Asn	GGA Gly 405	GCC Ala	CAG Gln	ATG Met	GAG Glu	AAA Lys 410	ATA Ile	CCC Pro	CTA Leu	TTG Leu	CAT His 415	ATT Ile	TCT Ser	TCA Ser	TGT Cys	1485
GAC Asp 420	CAA Gln	AAT Asn	ATT Ile	TCA Ser	GAA Glu 425	AAA Lys	GAC Asp	CTA Leu	Leu	GAC Asp 430	ACA Thr	GAG Glu	AAC Asn	AAA Lys	AGA Arg 435	1533
AAG Lys	AAA Lys	GAT Asp	TTT Phe	CTT Leu 440	ACT Thr	TCA Ser	GAG Glu	Asn	TCT Ser 445	TTG Leu	CCA Pro	CGT Arg	ATT Ile	TCT Ser 450	AGC Ser	1581
CTA	CCA	AAA	TCG	GAG	AAG	CCA	TTA	AAT (GAG (GAA .	ACA (GTG	GTA	AAT	AAG	1629

Le	u Pr	о Ly	s Se 45	r Gl 5	u Ly	s Pr	o Le	u As: 46		u Gl	u Th	r Va	l Va 46		n Lys	
AG Ar	A GA' g As	r GA o Gl 47	u GI	G CA u Gl	G CA n Hi	T CT s Le	T GA. u Gl: 47	u Se	T CA'	r AC	A GA r As	C TG p Cy 48	s Il	T CT' e Le	T GCA u Ala	1677
GT. Va	A AA(l Ly: 485	3 GT	G GC n Al	A AT. a Il	A TC	T GG r Gl 49	y Thi	T TC: r Se:	F CCA	A GTO Val	G GC' l Ala 49!	a Se	T TC: r Se:	A TT	r CAG e Gln	1725
GG: Gl ₃ 500	, ττε	C AA	A AA	G TC' s Se:	T ATA	∍ Ph	C AGA	A ATA	A AGA	GAZ Glu 510	ı Sei	A CC	r AA2 o Lys	A GAC	G ACT Thr 515	1773
TT(Phe	C AAT	GCA Ala	A AG	T TT: c Phe 520	e Sei	A GG	r CAT Y His	T ATO	ACT Thr	Asp	CCA Pro	A AAC Asr	TTT Phe	T AAA E Lys 530	AAA Lys	1821
GAA Glu	ACT Thr	GAA Glu	A GCC 1 Ala 535	ı Ser	GAA	A AGT	GGA Gly	CTG Leu 540	Glu	ATA Ile	CAT His	ACT Thr	GTT Val	. Cys	TCA Ser	1869
CAG Gln	AAG Lys	GAG Glu 550	Asp	TCC Ser	TTA Leu	TG1 Cys	CCA Pro 555	Asn	TTA Leu	ATT	GAT Asp	AAT Asn 560	Gly	AGC Ser	TGG Trp	1917
CCA Pro	GCC Ala 565	ACC Thr	ACC Thr	ACA Thr	CAG Gln	AAT Asn 570	Ser	GTA Val	GCT Ala	TTG Leu	AAG Lys 575	AAT Asn	GCA Ala	GGT Gly	TTA Leu	1965
ATA Ile 580	TCC Ser	ACT Thr	TTG Leu	AAA Lys	AAG Lys 585	AAA Lys	ACA Thr	AAT Asn	AAG Lys	TTT Phe 590	ATT Ile	TAT Tyr	GCT Ala	ATA Ile	CAT His 595	2013
GAT Asp	GAA Glu	ACA Thr	TCT Ser	TAT Tyr 600	AAA Lys	GGA Gly	AAA Lys	AAA Lys	ATA Ile 605	CCG Pro	AAA Lys	GAC Asp	CAA Gln	AAA Lys 610	TCA Ser	2061
GAA Glu	CTA Leu	ATT Ile	AAC Asn 615	TGT Cys	TCA Ser	GCC Ala	CAG Gln	TTT Phe 620	GAA Glu	GCA Ala	AAT Asn	GCT Ala	TTT Phe 625	GAA Glu	GCA Ala	2109
CCA Pro	CTT Leu	ACA Thr 630	TTT Phe	GCA Ala	AAT Asn	GCT Ala	GAT Asp 635	TCA Ser	GGT Gly	TTA Leu	TTG Leu	CAT His 640	TCT Ser	TCT Ser	GTG Val	2157
AAA Lys	AGA Arg 645	AGC Ser	TGT Cys	TCA Ser	CAG Gln	AAT Asn 650	GAT Asp	TCT Ser	GAA Glu	Glu	CCA Pro 655	ACT Thr	TTG Leu	TCC Ser	TTA Leu	2205
ACT	AGC	TCT	TTT	GGG	ACA	ATT	CTG	AGG .	AAA '	TGT	TCT .	AGA	AAT	GAA .	ACA	2253

Thr 660	Se	r Se	r Ph	e Gl	y Th 66	r Il. 5	e Le	ı Ar	g Ly	s Cy 67		r Ar	g As	n Gl	u Thr 675	
TGI Cys	Se:	r Aa c As	T AA' n As:	T AC	r Va	A ATO	C TC:	CAC	G GA' n Asj 68	p Le	r GA' u Asj	TA'	r AA.	A GAZ S Gli 690	A GCA 1 Ala 0	2301
AAA Lys	TG: Cys	ΓAA' SAS	T AA(n Ly:	s Glu	A AA 1 Ly:	A CTA	A CAC	TT2 Let 700	ı Phe	F AT: € Ile	r AC(C CCA	A GAZ O Gli 70!	ı Ala	GAT Asp	2349
TCT Ser	CTC	TC Sei 710	r Cys	C CTC	G CAC	G GAZ	A GGA Gly 715	Glr	TGT Cys	Γ GA <i>l</i> 3 Glι	A AAT 1 Asr	GAT Asp 720	Pro	A AAA	A AGC S Ser	2397
AAA Lys	AAA Lys 725	va.	TCA Ser	A GAT	ATA Ile	A AAA E Lys 730	Glu	GAG Glu	GTC Val	TTG Lev	GCT Ala 735	Ala	GCA Ala	TGT Cys	CAC His	2445
CCA Pro 740	GTA Val	. CAA	A CAC	TCA Ser	AAA Lys 745	Val	GAA Glu	TAC Tyr	AGT Ser	GAT Asp	Thr	GAC Asp	TTT Phe	CAA	TCC Ser 755	2493
CAG Gln	AAA Lys	AGT Ser	CTT Leu	TTA Leu 760	TAT Tyr	GAT Asp	CAT His	GAA Glu	AAT Asn 765	Ala	AGC Ser	ACT Thr	CTT Leu	ATT Ile 770	TTA Leu	2541
ACT Thr	CCT Pro	ACT Thr	TCC Ser 775	AAG Lys	GAT Asp	GTT Val	CTG Leu	TCA Ser 780	AAC Asn	CTA Leu	GTC Val	ATG Met	ATT Ile 785	TCT Ser	AGA Arg	2589
GGC Gly	AAA Lys	GAA Glu 790	TCA Ser	TAC Tyr	AAA Lys	ATG Met	TCA Ser 795	GAC Asp	AAG Lys	CTC Leu	AAA Lys	GGT Gly 800	AAC Asn	AAT Asn	TAT Tyr	2637
GAA Glu	TCT Ser 805	GAT Asp	GTT Val	GAA Glu	TTA Leu	ACC Thr 810	AAA Lys	AAT Asn	ATT Ile	CCC Pro	ATG Met 815	GAA Glu	AAG Lys	AAT Asn	CAA Gln	2685
GAT Asp 820	GTA Val	TGT Cys	GCT Ala	TTA Leu	AAT Asn 825	GAA Glu	AAT Asn	TAT Tyr	AAA Lys	AAC Asn 830	GTT Val	GAG Glu	CTG Leu	TTG Leu	CCA Pro 835	2733
CCT (GAA Glu	AAA Lys	TAC Tyr	ATG Met 840	AGA Arg	GTA Val	GCA Ala	TCA Ser	CCT Pro 845	TCA Ser	AGA Arg	AAG Lys	GTA Val	CAA Gln 850	TTC Phe	2781
AAC (Asn (CAA Gln	AAC Asn	ACA Thr 855	AAT Asn	CTA Leu	AGA Arg	Val	ATC Ile 860	CAA Gln	AAA Lys	AAT Asn	Gln	GAA Glu 865	GAA Glu	ACT Thr	2829
ACT T	CA	ATT	TCA	AAA	ATA	ACT	GTC .	AAT	CCA	GAC	TCT	GAA	GAA	CTT	TTC	2877

Thi	r Sei	87	e Se O	r Ly	s Il	e Th	r Val 875	l Ası 5	n Pr	o As	p Se	r Glu 880		u Lei	ı Phe	
TC <i>l</i> Ser	A GAC Asp 885	ASI	r ga n Gl	G AA u As:	T AA n As	T TT' n Phe 890	e Val	C TT(C CA.	A ATA	A GC' B Ala	a Asn	GAZ	A AGO u Ar <u>o</u>	G AAT J Asn	2925
AAT Asn 900	ı beu	GCT Ala	TTZ a Lei	A GG u Gl	A AA Y As: 90	n Thi	r AAG Lys	G GAA	A CT	T CAT 1 His 910	3 Gli	A ACA ı Thr	GA(C TTO	ACT Thr 915	2973
TGT Cys	' GTA Val	AAC Asn	GA Glu	A CC0 1 Pro 920) TT6	T TTC	AAG Lys	AAC Asn	TCT Ser 925	: Thr	ATC Met	GTT: Val	TTA Leu	A TAT I Tyr 930	GGA Gly	3021
GAC Asp	ACA Thr	GGT Gly	GAT Asp 935	, пле	A CAZ S Glr	A GCA n Ala	ACC Thr	CAA Gln 940	. Val	TCA Ser	ATT	' AAA : Lys	AAA Lys 945	Asp	TTG Leu	3069
GTT Val	TAT Tyr	GTT Val 950	CTT Leu	GCA Ala	GAG Glu	GAG Glu	AAC Asn 955	AAA Lys	AAT Asn	'AGT Ser	GTA Val	AAG Lys 960	CAG Gln	CAT His	ATA Ile	3117
AAA Lys	ATG Met 965	ACT Thr	CTA Leu	GGT Gly	CAA Gln	GAT Asp 970	TTA Leu	AAA Lys	TCG Ser	GAC Asp	ATC Ile 975	TCC Ser	TTG Leu	AAT Asn	ATA Ile	3165
GAT Asp 980	AAA Lys	ATA Ile	CCA Pro	GAA Glu	AAA Lys 985	AAT Asn	AAT Asn	GAT Asp	TAC Tyr	ATG Met 990	GAC Asp	AAA Lys	TGG Trp	GCA Ala	GGA Gly 995	3213
CTC Leu	TTA Leu	GGT Gly	PLO	ATT Ile 1000	TCA Ser	AAT Asn	CAC His	Ser	TTT Phe .005	GGA Gly	GGT Gly	AGC Ser	Phe	AGA Arg	ACA Thr	3261
GCT Ala	TCA . Ser .	ASII	AAG Lys 015	GAA Glu	ATC Ile	AAG Lys	Leu	TCT Ser 020	GAA Glu	CAT His	AAC Asn	ATT . Ile :	AAG Lys 025	AAG Lys	AGC Ser	3309
AAA . Lys	MEC.	TTC Phe 030	TTC Phe	AAA Lys	GAT Asp	Tle	GAA (Glu (035	GAA Glu	CAA Gln	TAT Tyr	Pro	ACT I	AGT Ser	TTA Leu .	GCT Ala	3357
TGT (Cys 1	GTT (Val (045	BAA . Blu	ATT Ile	GTA Val	Asn	ACC Thr	TTG (Leu <i>l</i>	GCA ' Ala 1	TTA Leu	Asp .	AAT Asn 055	CAA A Gln I	AAG Lys	AAA (Lys)	CTG Leu	3405
AGC A Ser I 1060	AAG (Lys I	CT (CAG Gln	ser	ATT Ile 065	AAT A	ACT (Thr \	GTA 1	Ser .	GCA (Ala 1 070	CAT '	TTA (Leu G	AG A	Ser S	AGT Ser)75	3453
GTA G	FTT G	TT 7	CT (GAT '	TGT .	AAA A	AAT A	AGT (CAT A	ATA A	ACC (CCT C	AG A	ATG T	TA	3501

Va:	l Va	l Va:	l Ser	1080	Cys	5 Lys	s Asr	ı Sei	r Hi:		e Thi	r Pro	o Gli	n Me	t Leu 0	
TTT Phe	TC Se:	C AAG	G CAG Glr 1095	ı Asp	TTT Phe	AAT Asn	TCA Ser	AAC Asr	ı His	r aa' s ası	T TTA	A ACA	A CC Pro 1105	Se:	C CAA r Gln	354
AAG Lys	GC Ala	A GAZ a Glu 1110	1 TTe	' ACA Thr	GAA Glu	CTI Leu	TCT Ser	Thr	T ATA	A TTA	A GAA 1 Glu	GAZ Glu 1120	Ser	A GG	A AGT y Ser	359
GII	TT: Phe 1125	e Glu	TTT Phe	ACT Thr	Gln	TTT Phe 1130	AGA Arg	AAA Lys	CCA Pro	AGO Ser	TAC Tyr 1135	Ile	TTG Leu	Glr	AAG Lys	364
AGT Ser 1140	AC <i>T</i> Thr	TTT Phe	GAA Glu	Val	CCT Pro 1145	GAA Glu	AAC Asn	CAG Gln	Met	ACT Thr	·Ile	TTA Leu	AAG Lys	ACC Thr	C ACT Thr 1155	3693
TCT Ser	GAG Glu	GAA Glu	Cys	AGA Arg 1160	GAT Asp	GCT Ala	GAT Asp	Leu	CAT His 1165	GTC Val	ATA	ATG Met	Asn	GCC Ala 1170	CCA Pro	374]
TCG Ser	ATT	GIA	CAG Gln 1175	GTA Val	GAC Asp	AGC Ser	Ser	AAG Lys 1180	CAA Gln	TTT Phe	GAA Glu	Gly	ACA Thr 1185	GTT Val	GAA Glu	3789
ATT Ile	цуѕ	CGG Arg 1190	AAG Lys	TTT Phe	GCT Ala	GTA	CTG Leu 195	TTG Leu	AAA Lys	AAT Asn	GAC Asp	TGT Cys L200	AAC Asn	AAA Lys	AGT Ser	3837
Ата	TCT Ser 205	GGT Gly	TAT Tyr	TTA Leu	Thr	GAT Asp .210	GAA Glu	AAT Asn	GAA Glu	Val	GGG Gly 1215	TTT Phe	AGG Arg	GGC Gly	TTT Phe	3885
TAT Tyr 220	TCT Ser	GCT Ala	CAT His	Gly	ACA Thr 225	AAA Lys	CTG Leu	AAT Asn	Val	TCT Ser .230	ACT Thr	GAA Glu	GCT Ala	Leu	CAA Gln 1235	3933
AAA Lys	GCT Ala	GTG Val	гуs	CTG Leu 240	TTT . Phe	AGT Ser	GAT Asp	Ile	GAG Glu 245	AAT Asn	ATT Ile	AGT Ser	Glu	GAA Glu 250	ACT Thr	3981
TCT Ser	GCA Ala	GIU	GTA (Val 1 255	CAT (CCA :	ATA :	Ser]	TTA Leu 260	TCT Ser	TCA Ser	AGT . Ser :	Lys	TGT Cys 265	CAT His	GAT Asp	4029
CT (Ser '	val	GTT Val :	TCA A	ATG : Met I	TTT A	Lys :	ATA (Ile (275	GAA 2 Glu 2	AAT Asn 1	CAT His	AAT (Asn 1	GAT Asp 1	AAA Lys	ACT Thr	GTA Val	4077
AGT (JAA .	AAA A	AAT A	AAT A	AAA T	rgc (CAA (CTG A	ATA '	TTA ·	CAA A	AAT 2	AAT .	ATT	GAA	4125

Ser	Glu 1285	Lys	Asn	Asn		Cys 1290	Gln	Leu	Ile		Gln 1295	Asn	Asn	Ile	Glu	
	ACT Thr			Thr					Ile					Lys		4173
	ACT Thr		Asn					Tyr					Arg			4221
	AAC Asn	Leu					Ser					Asn				4269
	ATT Ile					Thr					Thr					4317
Ile	TGT Cys 1365				Ser					Lys						4365
	AAA Lys			Leu					Phe					Lys		4413
	GAA Glu		Cys					Ser					Leu			4461
	AAA Lys	Thr					Lys					Ser				4509
	CAG Gln					Lys					Ala					4557
Asn	AAA Lys 1445				Phe					Pro					AAC Asn	4605
	TCC Ser			Ser					Asp					Lys		4653
	ATT Ile		Ser					Asp					Lys			4701
מ מ מ	GAA	ΔCT	GTC	CCD	CTTT	CCT	7 CT	GCIA	7.7.77	~~~		CTC	7 00	mma	a»a	4740

Lys	Glu	Ser	Val 1495	Pro	Val	Gly		Gly 1500	Asn	Gln	Leu		Thr 1505	Phe	Gln	
	Gln	CCC Pro 1510				Glu					Pro					4797
Phe		ACA Thr			Gly					Ile						4845
		GTG Val		Asn					Lys					Ser		4893
		AGT Ser	Phe					Ala					Tyr			4941
		AAA Lys					Ala					Glu				4989
	Pro	AAG Lys 1590				Met					Asn					5037
Leu		TCT Ser			Thr					Lys						5085
		AGA Arg		Thr					Thr					Phe		5133
		AAA Lys	Val					Glu					Lys			5181
		TGT Cys 1					Ser					Ile				5229
	Leu	GCT Ala .670				Ser					Thr					5277
Thr		TTA Leu			Ala					Arg						5325
GGT	CAA	CCA	GAA	AGA	ATA	AAT	ACT	GCA	GAT	TAT	GTA	GGA	AAT	TAT	TTG	5373

	Leu 1715	-	Asn	Gly		Tyr 1710		Ala	Thr		Ile 1705		Glu	Pro	Gln	Gly 1700
5421	CAT His		Lys					Ile			Asn		Asn			
5469	AAC Asn			Ser			Ser		Tyr					Glu		
5517	CTC Leu				Asp					Asp					Tyr	
5565	GTT Val					Pro					Asp					Ser
5613	AAA Lys 1795	Val					Lys					Asn	AAA Lys			
5661	GAG Glu		Cys					Val					Ala			
5709				Asn					Pro				ACT Thr 1815	Val		
5757	GCA Ala				Val					Ser			ATA Ile		Leu	
5805						Val					Gly		GCC Ala			Phe
5853	AAG Lys 1875	Ile	GTA Val	AAA Lys	AGT Ser	TTC Phe 1870	Ser	GAC Asp	ACA Thr	TTT Phe	ATA Ile 1865	Asp	AAA Lys	GTG Val	Lys AAA	AAA Lys 1860
5901			Ile					Ile					GAG Glu 1			
5949				Leu					Asp				GAG Glu .895	Tyr		
E007	C 7 C	CCT	uncom	Cum	7\ 7\ C	C 7 TP	ጥረአ	СУТ	ACG	ΔGC	ጥር:ጥ	GAA	GAT	ΤΑΔ	СЪТ	CTA

	Leu		Asn 1910		Glu	Сув		Thr 1915	His	Ser	His		Val 1920	Phe	Ala	Asp	
	Ile					Ile					Gln					. TTG Leu	6045
					Lys				TGT Cys	Asp					Thr	TCA Ser 1955	6093
				Lys		Ser			AAG Lys					Val			6141
			Thr					Ser	ACA Thr 1980				Lys				6189
		Ser					Gln		GCA Ala			Val					6237
	Glu					Gln			TCC Ser		Val						6285
					Gln				GAA Glu	Glu					Arg		6333
				Leu					GGC Gly					Val			6381
			Ala					Ser	ACA Thr 2060				Lys				6429
		Leu					His		GTT Val			Val					6477
1	Asp	TTA Leu 085	ATC Ile	AGA Arg	ACT Thr	Glu	CAT His 2090	AGT Ser	CTT Leu	CAC His	Tyr	TCA Ser 2095	CCT Pro	ACG Thr	TCT Ser	AGA Arg	6525
(CAA Gln 100	AAT Asn	GTA Val	TCA Ser	Lys	ATA Ile 2105	CTT Leu	CCT Pro	CGT Arg	Val	GAT Asp 2110	AAG Lys	AGA Arg	AAC Asn	Pro	GAG Glu 2115	6573
(מאַכי	тст	СΤЪ	AAC	тсъ	GNA	Δτιc	<i>ር</i> አ አ	7\7\7\	700	TICC	እ ሪ ሞ	71 71 71	C1 73 73	mmm	73 73 73	CC21

His	Сув	Val		Ser 2120	Glu	Met	Glu		Thr 2125	Суз	Ser	Lys		Phe 2130	Lys	
		AAT Asn					Glu					Glu				6669
	Ile	AAA Lys 2150	_			Tyr					Gln					6717
Gln		GTA Val			Thr					Val						6765
		AAA Lys		Gln					Asn					Ile		6813
		GAA Glu	Thr					Pro					Ile			6861
		ACT Thr					Ser					Glu				6909
	Glu	ATT Ile 2230				Phe					Glu					6957
Lys		CCA Pro			Ala					Phe						7005
		ATG Met		Leu					Ile				-	Gly		7053
		ATC Ile														7101
				2280	Cly	Oru	110		2285	дув	**** 5	ASII		2290	Apii	
_	TTT	GAC Asp	AGG	2280 ATA	ATA	GAA	AAT Asn	CAA	2285 GAA	AAA	TCC	TTA Leu	AAG	2290 GCT	TCA	7149
Glu AAA	TTT Phe AGC Ser	GAC Asp	AGG Arg 295 CCA	ATA Ile GAT	ATA Ile	GAA Glu ACA Thr	AAT Asn 2 ATA	CAA Gln 2300 AAA	GAA Glu GAT	AAA Lys CGA	TCC Ser AGA Arg	TTA Leu 2 TTG	AAG Lys 2305 TTT	GCT Ala ATG	TCA Ser	7149 7197

	Val 2325	Ser	Leu	Glu		Ile 2330	Thr	Cys	Val		Phe 2335	Arg	Thr	Thr	Lys	
				Ile					Phe		GCA Ala			Gln		7293
			Lys					Glu			ACT Thr		Glu			7341
		Asn					Gly				TAT Tyr	Gln				7389
	Arg					Arg					ACA Thr					7437
Lys					Pro					Ser	CAT His 2415					7485
				Arg					Glu		AAC Asn			Lys		7533
			Gly					Asp			AAT Asn		Ile			7581
		Ile					Lys				AAT Asn	Gln				7629
	Thr					Glu					GAT Asp					7677
Leu					Asp					Arg	ATT Ile 2495					7725
				Phe					Ser		TAT Tyr			ГЛа		7773
			Pro					Lys			GTA Val		Gly			7821
CCC	TCT	GCG	TGT	TCT	CAT	AAA	CAG	CTG	TAT	ACG	TAT	GGC	GTT	TCT	AAA	7869

Pro	Ser		Cys 2535	Ser	His	Lys		Leu 2540	Tyr	Thr	Tyr		Val 2545	Ser	Lys	
	Cys					Ser					TCT Ser					7917
Thr					${\tt Gly}$					Trp	ACT Thr 2575					7965
				Gly					Pro		AAT Asn			Lys		8013
			Glu					Leu			ACT Thr		Gly			8061
		Leu					${\tt Trp}$				CAC His	Tyr				8109
	Trp					Met					CCT Pro					8157
Asn					Pro					Leu	CAA Gln 2655					8205
				Ile					Arg		GCT Ala			Lys		8253
			Asp					Lys			GTT Val		Cys			8301
		Ile					Asn				ACT Thr	Ser				8349
	Ser					Gln					ATT Ile					8397
${ t Gly}$					Lys					Pro	CCC Pro					8445
TTA	AAG	AAT	GGC	AGA	CTG	ACA	GTT	GGT	CAG	AAG	ATT	ATT	CTT	CAT	GGA	8493

Leu 2740	Lys	Asn	Gly		Leu 2745	Thr	Val	Gly		Lys 2750	Ile	Ile	Leu		Gly 2755	
_		CTG Leu	Val					Ala					Glu			8541
		CTT Leu					Ser					Arg				8589
	Tyr	ACC Thr 2790				Phe					Arg					8637
Pro		TCA Ser			Phe					Asn						8685
		ATT Ile		Arg					Gln					Thr		8733
		TTA Leu	Tyr					Glu					Lys			8781
		TAT Tyr					Gln					Ala				8829
	Ile	CAG Gln 2870				Glu					Asn					8877
Tyr		CCA Pro			Ala					Gln						8925
		GCA Ala		Leu					Lys					Pro		8973
		GAG Glu	Gly					Glu					Leu			9021
		CAA Gln					Lys					Ile				9069
ATT	AGG	AAG	ACC	ATG	GAA	TCT	GCT	GAA	CAA	AAG	GAA	CAA	GGT	TTA	TCA	9117

Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser 2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys 2965 2970 2975	9165
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp 2980 2985 2990 2995	9213
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu 3000 3005 3010	9261
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA Ala Thr Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu 3015 3020 3025	9309
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu 3030 3035 3040	9357
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045 3050 3055	9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060 3065 3070 3075	9453
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080 3085 3090	9501
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3095 3100 3105	9549
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3110 3115 3120	9597
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125 3130 3135	9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe 3140	9693

Gln	Glu	Thr		Asn 3160	Lys	Met	Lys		Thr 3165	Val	Glu	Asn		Asp 3170	Ile	
		AAT Asn					Lys					Leu				9789
	Pro	AAG Lys 3190				Pro					Thr					9837
Thr		CAA Gln			Pro					Lys						9885
		TGT Cys		Ile					Pro					Met		9933
		AAG Lys	Ser					Val					Thr			9981
		AAA Lys					Ile					Asn				10029
	Arg	GCC Ala 3270				Leu					Leu					10077
Ser		ATT Ile			Phe					Ala						10125
		AGG Arg		Cys					Glu					Lys		10173
		AAT Asn	Ser					Pro					Asn			10221
		TTG Leu 3					Ile					Leu				10269
	Thr	CAA Gln 3350				Ser					Glu					10317
TCT	GTC	AGT	GAA	TCC	ACT	AGG	ACT	GCT	CCC	ACC	AGT	TCA	GAA	GAT	TAT	10365

Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 3375

CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu 3380 3395 3390 3395

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA Ile Thr Thr Lys Lys Tyr Ile 3415

10485

- (2) INFORMATION FOR SEQ ID NO:13:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys 10 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe 25 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile 75 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys 90 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser 105 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp 120 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val 135 140 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val 150 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr 170 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met

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180
                                185
                                                     190
Ser Trp Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
                            200
Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
                        215
                                            220
Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
                    230
                                        235
Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
                                    250
Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
                                265
Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
                            280
His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
                        295
Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
                    310
                                        315
Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
                325
                                    330
Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
            340
                                345
Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
                            360
Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
                        375
                                            380
Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
                    390
                                        395
Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
                405
                                    410
Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
            420
                                425
Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
                            440
                                                445
Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
                        455
Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
                    470
                                        475
Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
                                    490
Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
            500
                                505
Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
                            520
Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
                        535
                                            540
Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
                    550
                                        555
Gly Ser Trp Pro Ala Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
               565
                                    570
Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
                                585
Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
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Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Ile Ala Asn Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile

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1010
                        1015
                                            1020
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
                   1030
                                        1035
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
                1045
                                   1050
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
            1060
                               1065
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
        1075
                           1080
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
                        1095
                                            1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
                    1110
                                        1115
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
                1125
                                   1130
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
            1140
                               1145
                                                   1150
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
        1155
                           1160
                                               1165
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
                       1175
                                           1180
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
                   1190
                                       1195
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
                1205
                                   1210
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
            1220
                                1225
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
                           1240
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Lys
                       1255
                                           1260
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
                    1270
                                      1275
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
               1285
                                   1290
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
           1300
                               1305
                                                   1310
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
                           1320
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
                       1335
                                           1340
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
                   1350
                                      1355
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
               1365
                                   1370
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
           1380
                               1385
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
                           1400
                                              1405
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
                       1415
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
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1425
                   1430
                                       1435
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
               1445
                                  1450
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
           1460
                              1465
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
                 1480
                                             1485
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
                      1495
                                          1500
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
                   1510
                                       1515
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
               1525
                                   1530
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
            1540
                       1545
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
                          1560
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
                       1575
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
                   1590
                                     1595
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
               1605
                                  1610
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
                               1625
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
                           1640
                                              1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
                       1655
                                          1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
                   1670
                                      1675
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
              1685
                                 1690
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
           1700
                    1705
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
       1715
                         1720
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
                       1735
                                          1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
                   1750
                                      1755
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
               1765
                                 1770
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
                              1785
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
                         1800
                                             1805
Cys Val Glu Glu Leu Val Thr Ser Ser Pro Cys Lys Asn Lys Asn
                      1815
                                          1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
                  1830
                                     1835
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
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Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg

			226					226					227		
Arg	Gly	Glu 227		Lei	ı Ile	e Lei	ı Val		Glı	ı Pro	Ser	11e	_	arg	Asr
Leu	Leu 229	Asn 0	Glu	Phe	e Asp	229		e Ile	Glı	ı Asn	Gln 230	Glu		Ser	Leu
Lys 230	Ala 5	Ser	Lys	Ser	Thr 231) Asp	Gly	Thi	: Ile 231	Lys		Arg	Arg	Leu 232
Phe	Met	His	His	Val 232		Leu	ı Glu	ı Pro	11e	Thr		Val	Pro	Phe	Arg
Thr	Thr	Lys	Glu 234	Arg		ı Glu	ılle	Gln 234	Asr		Asn	Phe		233 Ala	Pro
Gly	Gln	Glu 235	Phe		ı Ser	Lys		His		ı Tyr	Glu			Thr	Leu
Glu	Lys	Ser		Ser	Asn				Ser	Gly				Tyr	Gln
			Thr	Arg	Asn	237 Glu		Met	Arg				Thr	Thr	Gly
238! Arg		Thr	Lys	Val	239 Phe		Pro	Pro	Phe	239 Lys		Lys	Ser	His	240 Phe
His	Arg	Val	Glu	240 Gln	-	Val	Arg	Asn	241 Ile		Leu	Glu	Glu	241 Asn	5 Ara
			242	0				242	5				243		
	_	243	5		_	4	244			12-		244		11011	y 5
Ile	Asn 2450	Asp	Asn	Glu	Ile	His 245		Phe	Asn	Lys	Asn 246	Asn	Ser	Asn	Gln
Ala 2465	Ala	Ala	Val	Thr	Phe 247		Lys	Cys	Glu	Glu 247	Glu		Leu	Asp	Leu 248
Ile	Thr	Ser	Leu	Gln 248	Asn		Arg	Asp	Ile 249	Gln		Met	Arg	Ile	Lys
Lys	Lys	Gln	Arg 250	Gln		Val	Phe	Pro 250!	Gln		Gly	Ser		249! Tyr	
Ala	Lys	Thr 2515	Ser		Leu	Pro		Ile		Leu	Lys			Val	Gly
Gly	Gln 2530	Val		Ser	Ala	Cys	252 Ser -		Lys	Gln				Tyr	Gly
Val			иiс	Ctra	т1.	253		71	a	T	2540		~ 7	~	_,
2545	;				255	0				2555	5			Ser	256
				256	5				257	0				Thr 2575	5
			2580)				2585	5				2590		
		2595	5				2600)				2605	5	Thr	
Gly	Val . 2610	Asp	Pro	Lys	Leu	Ile 261	Ser	Arg	Ile	Trp	Val 2620		Asn	His	Tyr
Arg 2625	Trp	Ile	Ile	Trp	Lys 2630	Leu)	Ala	Ala	Met	Glu 2635	Cys		Phe	Pro	Lys 264
Glu	Phe 2	Ala	Asn	Arg 2645	Cys	Leu	Ser	Pro	Glu 2650	Arg		Leu	Leu	Gln 2655	Leu
ŗÀz	Tyr I	Arg		Asp		Glu	Ile	Asp 2665	Arg		Arg	Arg	Ser 2670	Ala	Ile
Lys	Lys :				Arg	Asp	qaA			Ala	Lys	Thr	Leu	Val	Leu

Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys

	200	^					_								
1	309					309					310				
Pne	Trp	Ile	Asp	Leu	Asn	Glu	Asp	Ile	Ile	: Lys	Pro	His	Met	Leu	$I1\epsilon$
310					311					311					312
Ala	Ala	Ser	Asn	Leu	Gln	Trp	Arg	Pro	Glu	Ser	Lys	Ser	G1y	Leu	Let
				312	5				313	0				313	5
Thr	Leu	Phe	Ala	Gly	Asp	Phe	Ser	Val	Phe	Ser	Ala	Ser	Pro	Lvs	Glu
			314					314					315		
Gly	His	Phe	Gln	Glu	Thr	Phe	Asn	Lys	Met	Lvs	Asn	Thr	Val	G] 11	Δgr
		315	5				316		_	-1 -		316		O_u	1101
Ile	Asp			Cys	Asn	Glu			Agn	Lvg	T.e.ii			Tlo	T. 61
	317	0		- 2		317			11011	шуы	318		117.0	110	шес
His	Ala	Asn	Asn	Pro	Lvs			Thr	Dro	Thr	Larg	7 ~~	0	mb	0
318	 5		TTOP	110	319		DCI	1111	FLO	319		Asp	Сув	THE	
		Trz	Thr	777			T 1 -	Dana	a 1				_	_	320
Cry	110	TYT	T 11T	Ala		TIE	тте	PLO			GIY	Asn	гЛа		
Mot	0	G	_	320		~ 7		_	321					321	5
мес	ser	ser		Asn	Cys	Glu	IIe			Gln	Ser	Pro			Leu
~			322					322					323)	
Cys	Met	Ala	Lys	Arg	Lys	Ser			Thr	Pro	Val	Ser	Ala	Gln	Met
		323					324					324!	5		
Thr	Ser	Lys	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn
	325	0				325	5				326	0			
Cys	Lys	Lys	Arg	Arg	Ala	Leu	Asp	Phe	Leu	Ser	Arg	Leu	Pro	Leu	Pro
326	5				327					3275					328
Pro	Pro	Val	Ser	Pro	Ile	Cys	Thr	Phe	Val	Ser	Pro	Ala	Ala	Gln	
				3285		_			3290		_			3295	
Ala	Phe	Gln	Pro	Pro	Ara	Ser	Cvs	Glv			Tur	Glu	Thr		
			3300		3		0,70	330		цуь	+ 7 -	OIU	3310		TTC
Lvs	Lvs	Lvs		Leu	Δan	Ser	Dro			Thr	Dwo	Dhe			D1
-1-	-12	3315	5	u	71011	UCI	3320		Mec	TIIT	PIO			гув	Pne
Δan	Gl ₁₁		-	Lon	T 011	<i>α</i> 1			0	~ 7 -	- 7	3325			_
1011	3330	110	PET	Leu	цец			Asn	ser	тте			GLu	Glu	Leu
77 7			20	m1	٦.	3335		_	_	_	3340				
Ata Ata	ьeu	тте	Asn	Thr	GIN	Ala	Leu	Leu	Ser			Thr	Gly	Glu	Lys
3345 ~-					3350					3355					336
GIn	Phe	Ile	Ser	Val	Ser	Glu	Ser	Thr	Arg	Thr	Ala	Pro	Thr	Ser	Ser
				3365					3370					3375	5
Glu	Asp	Tyr	Leu	Arg	Leu	Lys	Arg	Arg	Cys	Thr	Thr	Ser	Leu	Ile	Lys
			3380)				3385					3390		4
Glu	Gln	Glu	Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cvs	Glu	Lvs	Asn	Lvs
		3395	i				3400				4	3405			-, 2
Gln	Asp	Thr	Ile	Thr	Thr	Lys	Lys	Tyr	Ile						
	3410					3415		- 1							

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:

(B) LOCATION: 120 (D) OTHER INFORMATION: 2F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
TGAGTTTTAC CTCAGTCACA	20
(2) INFORMATION FOR SEQ ID NO:15:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 41 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
CAGGAAACAG CTATGACCCT GTGACGTACT GGGTTTTTAG C	41
(2) INFORMATION FOR SEQ ID NO:16:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 120(D) OTHER INFORMATION: 3FII primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
GATCTTTAAC TGTTCTGGGT CACA	24
(2) INFORMATION FOR SEQ ID NO:17:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	

(B) LOCATION: 122 (D) OTHER INFORMATION: 3RII primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
CCCAGCATGA CACAATTAAT GA	22
(2) INFORMATION FOR SEQ ID NO:18:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 144(D) OTHER INFORMATION: 4F/M 13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
TGTAAAACGA CGGCCAGTAG AATGCAAATT TATAATCCAG AGTA	44
(2) INFORMATION FOR SEQ ID NO:19:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 122(D) OTHER INFORMATION: 4R-1A primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
ATCAGATTCA TCTTTATAGA AC	22

(ix) FEATURE

(A) LENGTH: 40 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 140 (D) OTHER INFORMATION: 5+6F/M13F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
TGTAAAACGA CGGCCAGTTG TGTTGGCATT TTAAACATCA	40
(2) INFORMATION FOR SEQ ID NO:21:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 138(D) OTHER INFORMATION: 5+6R/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
CAGGAAACAG CTATGACCCA GGGCAAAGGT ATAACGCT	38
(2) INFORMATION FOR SEQ ID NO:22:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA	
(,	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(ix) FEATURE	
(A) NAME/KEY: other(B) LOCATION: 138(D) OTHER INFORMATION: 7F/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
TGTAAAACGA CGGCCAGTTA AGTGAAATAA AGAGTGAA	38
(2) INFORMATION FOR SEQ ID NO:23:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 36 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 136 (D) OTHER INFORMATION: 7R/M13R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
CAGGAAACAG CTATGACCAG AAGTATTAGA GATGAC	36
(2) INFORMATION FOR SEQ ID NO:24:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 40 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 140(D) OTHER INFORMATION: 8F/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	

TGTAAAACGA CGGCCAGTGC CATATCTTAC CACCTTGTGA

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ix) FEATURE:	
(A) NAME/KEY: other (B) LOCATION: 122 (D) OTHER INFORMATION: 8FIA primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
TTGCATTCTA GTGATAATAT AC	22
(2) INFORMATION FOR SEQ ID NO:26:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 119(D) OTHER INFORMATION: 8RIA primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
AATTGTTAGC AATTTCAAC	19
(2) INFORMATION FOR SEQ ID NO:27:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	

(2) INFORMATION FOR SEQ ID NO:25:

(B) LOCATION: 140 (D) OTHER INFORMATION: 9F/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
TGTAAAACGA CGGCCAGTTG GACCTAGGTT GATTGCAGAT	40
(2) INFORMATION FOR SEQ ID NO:28:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 140(D) OTHER INFORMATION: 9R/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
CAGGAAACAG CTATGACCTA AACTGAGATC ACGGGTGACA	40
(2) INFORMATION FOR SEQ ID NO:29:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 124 (D) OTHER INFORMATION: 10AF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
GAATAATATA AATTATATGG CTTA	24
(2) INFORMATION FOR SEQ ID NO:30:	

(A) LENGTH: 37 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other(B) LOCATION: 137(D) OTHER INFORMATION: 10AR/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
CAGGAAACAG CTATGACCCC TAGTCTTGCT AGTTCTT	37
(2) INFORMATION FOR SEQ ID NO:31:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other(B) LOCATION: 142(D) OTHER INFORMATION: 10BF/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
TGTAAAACGA CGGCCAGTAR CTGAAGTGGA ACCAAATGAT AC	42
(2) INFORMATION FOR SEQ ID NO:32:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 44 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	

(i) SEQUENCE CHARACTERISTICS:

(D) OTHER INFORMATION: 10BR/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
CAGGAAACAG CTATGACCAC GTGGCAAAGA ATTCTCTGAA GTAA	44
(2) INFORMATION FOR SEQ ID NO:33:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 40 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ix) FEATURE:	
(ii) MOLECULE TYPE: Genomic DNA	
(A) NAME/KEY: other(B) LOCATION: 140(D) OTHER INFORMATION: 10CF/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
TGTAAAACGA CGGCCAGTCA GCATCTTGAA TCTCATACAG	40
(2) INFORMATION FOR SEQ ID NO:34:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 19 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 119 (D) OTHER INFORMATION: 10CRII primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
AGACAGAGGT ACCTGAATC	19
(2) INFORMATION FOR SEC ID MO.35.	

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 140(D) OTHER INFORMATION: 11AF-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
TGTAAAACGA CGGCCAGTTG GTACTTTAAT TTTGTCACTT	40
(2) INFORMATION FOR SEQ ID NO:36:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 37 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 137(D) OTHER INFORMATION: 11AR-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
CAGGAAACAG CTATGACCTG CAGGCATGAC AGAGAAT	37
(2) INFORMATION FOR SEQ ID NO:37:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 40 base pairs

(B) LOCATION: 122 (D) OTHER INFORMATION: 11BF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
AAGAAGCAAA ATGTAATAAG GA	22
(2) INFORMATION FOR SEQ ID NO:38:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 122 (D) OTHER INFORMATION: 11BR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
CATTTAAAGC ACATACATCT TG	22
(2) INFORMATION FOR SEQ ID NO:39:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: primer(B) LOCATION:(D) OTHER INFORMATION: 11CF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
TCTAGAGGCA AAGAATCATA C	21
(2) INFORMATION FOR SEQ ID NO:40:	

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other(B) LOCATION: 122(D) OTHER INFORMATION: 11CR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
CAAGATTATT CCTTTCATTA GC	22
(2) INFORMATION FOR SEQ ID NO:41:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 122(D) OTHER INFORMATION: 11DF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
AACCAAAACA CAAATCTAAG AG	22
(2) INFORMATION FOR SEQ ID NO:42:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs

(A) NAME/KEY: other	
(B) LOCATION: 123	
(D) OTHER INFORMATION: 11DR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
GTCATTTTTA TATGCTGCTT TAC	23
(2) INFORMATION FOR SEQ ID NO:43:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 121	
(D) OTHER INFORMATION: 11EF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
GGTTTTATAT GGAGACACAG G	21
(2) INFORMATION FOR SEQ ID NO:44:	
(2) INTORMATION FOR DEG ID NO. 44.	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(b) Torollogi. Timedi	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 123	
(D) OTHER INFORMATION: 11ER primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:	
GTATTTACAA TTTCAACACA AGC	23
(2) INFORMATION FOR SEQ ID NO:45:	

(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 120(D) OTHER INFORMATION: 11FF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
ATCACAGTTT TGGAGGTAGC	20
(2) INFORMATION FOR SEQ ID NO:46:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 121 (D) OTHER INFORMATION: 11FR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
CTGACTTCCT GATTCTTCTA A	21
(2) INFORMATION FOR SEQ ID NO:47:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	

(i) SEQUENCE CHARACTERISTICS:

(B) LOCATION: 121 (D) OTHER INFORMATION: 11GF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
CTCAGATGTT ATTTTCCAAG C	21
(2) INFORMATION FOR SEQ ID NO:48:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 121(D) OTHER INFORMATION: 11GR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	
CTGTTAAATA ACCAGAAGCA C	21
(2) INFORMATION FOR SEQ ID NO:49:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 18 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 118(D) OTHER INFORMATION: 11HF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	
AGGTAGACAG CAGCAAGC	18
(2) INFORMATION FOR SEQ ID NO:50:	

(A) NAME/KEY: other

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 22 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ix) FEATURE:	
(A) NAME/KEY: other	
(B) LOCATION: 122	
(D) OTHER INFORMATION: 11HR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	
GTAATATCAG TTGGCATTTA TT	22
(2) INFORMATION FOR SEQ ID NO:51:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(A) NAME/KEY: other	
(B) LOCATION: 121	
(D) OTHER INFORMATION: 111F primer	
(b) office information. Till primer	
(and) GROUPINGE PROGRESSION GROUP AND AN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
TGCAGAGGTA CATCCAATAA G	21
TOCHOLOGIA CATCCAMIAA U	21
(2) INFORMATION FOR SEQ ID NO:52:	
~	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLEGILE TWDE Company's Torr	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	

(B) LOCATION: 1...21

(D) OTHER INFORMATION: 11IR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
GATCAGTAAA TAGCAAGTCC G	21
(2) INFORMATION FOR SEQ ID NO:53:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 123(D) OTHER INFORMATION: 11JF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
TACTGAAAAT GAAGATAACA AAT	23
(2) INFORMATION FOR SEQ ID NO:54:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 122 (D) OTHER INFORMATION: 11JR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
ATTTTGTTCT TTCTTATGTC AG	22
(2) INFORMATION FOR SEQ ID NO:55:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 35 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 135(D) OTHER INFORMATION: 11KF-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA	35
(2) INFORMATION FOR SEQ ID NO:56:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 35 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(A) NAME/KEY: other(B) LOCATION: 135(D) OTHER INFORMATION: 11KR-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG	35
(2) INFORMATION FOR SEQ ID NO:57:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: Genomic DNA
 - (ix) FEATURE
 - (A) NAME/KEY: other
 - (B) LOCATION: 1...22
 - (D) OTHER INFORMATION: 11LF primer
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

(2) INFORMATION FOR SEQ ID NO:58:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 19 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 119(D) OTHER INFORMATION: 11LR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
GGCACCACAG TCTCAATAG	. 9
(2) INFORMATION FOR SEQ ID NO:59:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 11MF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
GCAAAGACCC TAAAGTACAG 2	0
(2) INFORMATION FOR SEQ ID NO:60:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

CACAAAATAC TGAAAGAAAG TG

(ix) FEATURE	
(A) NAME/KEY: other(B) LOCATION: 122(D) OTHER INFORMATION: 11MR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
CATCAAATAT TCCTTCTCA AG	22
(2) INFORMATION FOR SEQ ID NO:61:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other(B) LOCATION: 135(D) OTHER INFORMATION: 11NF-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
TGTAAAACGA CGGCCAGTGA AAATTCAGCC TTAGC	35
(2) INFORMATION FOR SEQ ID NO:62:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 135(D) OTHER INFORMATION: 11NR-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	

(ii) MOLECULE TYPE: Genomic DNA

CAGGAAACAG CTATGACCAT CAGAATGGTA GGAAT	35
(2) INFORMATION FOR SEQ ID NO:63:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 122(D) OTHER INFORMATION: 110F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
GTACTATAGC TGAAAATGAC AA	22
(2) INFORMATION FOR SEQ ID NO:64:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 120(D) OTHER INFORMATION: 110R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
ACCACTGGCT ATCCTAAATG	20
(2) INFORMATION FOR SEQ ID NO:65:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(A) NAME/KEY: other	
(B) LOCATION: 120 (D) OTHER INFORMATION: 11PF primer	
(b) Official Information. Tipp primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	
TGAAGATATT TGCGTTGAGG	20
(2) INFORMATION FOR GEO ID NO. CC	
(2) INFORMATION FOR SEQ ID NO:66:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 20 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 120	
(D) OTHER INFORMATION: 11PR primer	
(xi) SEOUENCE DESCRIPTION: SEO ID NO.66.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66: GTCAGCAAAA ACCTTATGTG	20
GTCAGCAAAA ACCTTATGTG	20
	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67:	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS:	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE	20
GTCAGCAAAA ACCTTATGTG (2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE (A) NAME/KEY: other	20
(2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 121	20
(2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 121 (D) OTHER INFORMATION: 11QF primer	20
(2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 121	20

(ii) MOLECULE TYPE: Genomic DNA

(2) INFORMATION FOR SEQ ID NO:68:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 121(D) OTHER INFORMATION: 11QR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
CTTGTCTTGC GTTTTGTAAT G	21
(2) INFORMATION FOR SEQ ID NO:69:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 11RF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
GCTTCATAAG TCAGTCTCAT	20
(2) INFORMATION FOR SEQ ID NO:70:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

ACGAAAATTA TGGCAGGTTG T

(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 120 (D) OTHER INFORMATION: 11RR primer	
(b) Ollille Intollillon. Finds primor	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
TCAAATTCCT CTAACACTCC	20
(2) INFORMATION FOR SEQ ID NO:71:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 35 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 135	
(D) OTHER INFORMATION: 11SF-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
TGTAAAACGA CGGCCAGTTA CAGCAAGTGG AAAGC	35
(2) INFORMATION FOR SEQ ID NO:72:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 37 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(2) 20202021 222001	
(ii) MOLECULE TYPE: Genomic DNA	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 137	
(D) OTHER INFORMATION: 11SR-M13 primer	

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
CAGGAAACAG CTATGACCAA GTTTCAGTTT TACCAAT	37
(2) INFORMATION FOR SEQ ID NO:73:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 122(D) OTHER INFORMATION: 11TF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
GTTCTTCAGA AAATAATCAC TC	22
(2) INFORMATION FOR SEQ ID NO:74:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 121 (D) OTHER INFORMATION: 11TR primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
TGTAAAAAGA GAATGTGTGG C	21
(2) INFORMATION FOR SEQ ID NO:75:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 139(D) OTHER INFORMATION: 11UF-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
TGTAAAACGA CGGCCAGTAC TTTTTCTGAT GTTCCTGTG	39
(2) INFORMATION FOR SEQ ID NO:76:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other(B) LOCATION: 139(D) OTHER INFORMATION: 11UR-M13 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
CAGGAAACAG CTATGACCTA AAAATAGTGA TTGGCAACA	39
(2) INFORMATION FOR SEQ ID NO:77:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 142(D) OTHER INFORMATION: 12F/M13F primer	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:	
TGTAAAACGA CGGCCAGTAG TGGTGTTTTA AAGTGGTCAA AA	42
(2) INFORMATION FOR SEQ ID NO:78:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 40 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 140 (D) OTHER INFORMATION: 12R/M13R primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:	
CAGGAAACAG CTATGACCGG ATCCACCTGA GGTCAGAATA	40
(2) INFORMATION FOR SEQ ID NO:79:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 121 (D) OTHER INFORMATION: 13-2F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	
TAACATTTAA GCATCCGTTA C	21
(2) INFORMATION FOR SEQ ID NO:80:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 128	
(D) OTHER INFORMATION: 13-2R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
AAACGAGACT TTTCTCATAC TGTATTAG	28
HAACGAGACI IIICICAIAC IGIAIIAG	20
(2) INFORMATION FOR SEQ ID NO:81:	
•	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 22 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 122	
(D) OTHER INFORMATION: 14F primer	
() GEOMENGE DEGGRIDATION, GEO. ID NO. 01.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
ACCATGTAGC AAATGAGGGT CT	22
(2) INFORMATION FOR SEQ ID NO:82:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 22 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 122 (D) OTHER INFORMATION: 14AP primer	
III DTHED INECONATION IZAD AYIMAY	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
GCTTTTGTCT GTTTTCCTCC AA	22
(2) INFORMATION FOR SEQ ID NO:83:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 121 (D) OTHER INFORMATION: 15-2F primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
CCAGGGGTTG TGCTTTTAA A	21
(2) INFORMATION FOR SEQ ID NO:84:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 38 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: primer(B) LOCATION:(D) OTHER INFORMATION: 15FUT/M13-R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
CAGGAAACAG CTATGACCAC TCTGTCATAA AAGCCATC	38
(2) INFORMATION FOR SEQ ID NO:85:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 124 (D) OTHER INFORMATION: 16AF primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
TTTGGTTTGT TATAATTGTT TTTA	24
(2) INFORMATION FOR SEQ ID NO:86:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other(B) LOCATION: 120(D) OTHER INFORMATION: 16AR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
CCAACTTTTT AGTTCGAGAG	20
(2) INFORMATION FOR SEQ ID NO:87:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 119(D) OTHER INFORMATION: 17F primer	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	
TTCAGTATCA TCCTATGTG	19
(2) INFORMATION FOR SEQ ID NO:88:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 120(D) OTHER INFORMATION: 17AR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:	
AGAAACCTTA ACCCATACTG	20
(2) INFORMATION FOR SEQ ID NO:89:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 139(D) OTHER INFORMATION: 18FUT/M13-AF primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:	
TGTAAAACGA CGGCCAGTGA ATTCTAGAGT CACACTTCC	39
(2) INFORMATION FOR SEQ ID NO:90:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 38 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 138(D) OTHER INFORMATION: 18R/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	
CAGGAAACAG CTATGACCTT TAACTGAATC AATGACTG	38
(2) INFORMATION FOR SEQ ID NO:91:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 41 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 141(D) OTHER INFORMATION: 19F/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:	
TGTAAAACGA CGGCCAGTAA GTGAATATTT TTAAGGCAGT T	41
(2) INFORMATION FOR SEQ ID NO:92:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE</pre>	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
CAGGAAACAG CTATGACCAA GAGACCGAAA CTCCATCTC	39
(2) INFORMATION FOR SEQ ID NO:93:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 38 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other(B) LOCATION: 138(D) OTHER INFORMATION: 20F/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
TGTAAAACGA CGGCCAGTCA CTGTGCCTGG CCTGATAC	38
(2) INFORMATION FOR SEQ ID NO:94:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 139(D) OTHER INFORMATION: 20R/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:	2.0
CAGGAAACAG CTATGACCAT GTTAAATTCA AAGTCTCTA	39
(2) INFORMATION FOR SEQ ID NO:95:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid	

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(II) MODECOLE TIPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 139 (D) OTHER INFORMATION: 21F/M13F primer	
(a) office and office	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
TGTAAAACGA CGGCCAGTGG GTGTTTTATG CTTGGTTCT	39
(2) INFORMATION FOR SEQ ID NO:96:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 40 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 140	
(D) OTHER INFORMATION: 21R/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:	
CAGGAAACAG CTATGACCCA TTTCAACATA TTCCTTCCTG	40
(2) INFORMATION FOR SEQ ID NO:97:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 19 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	

(C) STRANDEDNESS: single

(B) LOCATION: 119 (D) OTHER INFORMATION: 22F-1A primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:	
AACCACACCC TTAAGATGA	19
(2) INFORMATION FOR SEQ ID NO:98:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 22R-1A primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:	
GCATTAGTAG TGGATTTTGC	20
(2) INFORMATION FOR SEQ ID NO:99:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 16 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE(A) NAME/KEY: other(B) LOCATION: 116(D) OTHER INFORMATION: 23FII primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:	
TCACTTCCAT TGCATC	16
(2) INFORMATION FOR SEC ID NO.100.	

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 117 (D) OTHER INFORMATION: 23RII primer</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:	
TGCCAACTGG TAGCTCC	17
(2) INFORMATION FOR SEQ ID NO:101:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 24 2F primer	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 120</pre>	
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 24 2F primer</pre>	20
<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 24 2F primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:</pre>	20
(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 24 2F primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101: TACAGTTAGC AGCGACAAAA	20

(i) SEQUENCE CHARACTERISTICS:

(A) NAME/KEY: other	
(B) LOCATION: 138	
(D) OTHER INFORMATION: 24R/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:	
(XI) SEQUENCE DESCRIPTION. SEQ ID NO.102.	
CAGGAAACAG CTATGACCAT TTGCCAACTG GTAGCTCC	38
CAUDAMICAU CIMIUMCOMI IIUGGILICIO UMBOTO	00
(2) INFORMATION FOR SEQ ID NO:103:	
(-,	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 20 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 120	
(D) OTHER INFORMATION: 25F-7/23 primer	
() GEOLIENGE DECERTIONIC GEO ID NO. 102.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:	
GCTTTCGCCA AATTCAGCTA	20
GCTTCGCCA ANTICAGCTA	
(2) INFORMATION FOR SEQ ID NO:104:	
(2)	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 20 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE	
(A) NAME/KEY: other	
(B) LOCATION: 120	
(D) OTHER INFORMATION: 25R-7/23 primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	

(ix) FEATURE

TACCAAAATG TGTGGTGATG

20

(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 26-2F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:	
AATCACTGAT ACTGGTTTTG	20
(2) INFORMATION FOR SEQ ID NO:106:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 120 (D) OTHER INFORMATION: 26-2R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:	
TATACTTACA GGAGCCACAT	20
(2) INFORMATION FOR SEQ ID NO:107:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

<pre>(ix) FEATURE (A) NAME/KEY: other (B) LOCATION: 118</pre>	
(D) OTHER INFORMATION: 27AF-1A primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:	
CTGTGTGTAA TATTTGCG	18
(2) INFORMATION FOR SEQ ID NO:108:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 40 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE (A) NAME/KEY: other	
(B) LOCATION: 140 (D) OTHER INFORMATION: 27AR/M13R primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:	
CAGGAAACAG CTATGACGGC AAGTTCTTCG TCAGCTATTG	40
(2) INFORMATION FOR SEQ ID NO:109:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(ix) FEATURE (A) NAME/KEY: other	
(B) LOCATION: 140 (D) OTHER INFORMATION: 27BF/M13F primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:	

(ii) MOLECULE TYPE: Genomic DNA

TGTAAAACGA CGGCCAGTGA ATTCTCCTCA GATGACTCCA

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- (2) INFORMATION FOR SEQ ID NO:110:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 - (ix) FEATURE
 - (A) NAME/KEY: other
 - (B) LOCATION: 1...38
 - (D) OTHER INFORMATION: 27BR/M13R primer
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CAGGAAACAG CTATGACCTC TTTGCTCATT GTGCAACA

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- (2) INFORMATION FOR SEQ ID NO:111:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1...1158
 - (D) OTHER INFORMATION: Exon 10, nucleotides 31-1146 correspond to nucleotides 1022-2137 of complete coding sequence
- (ix) FEATURE
 - (A) NAME/KEY: variable
 - (B) LOCATION: 102...602
 - (D) OTHER INFORMATION: M at positions 102 or 351 = A or C; R at position 602 = A or G.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:
- TTAATGTGCT TCTGTTTTAT ACTTTAACAG GATTTGGAAA AACATCAGGG AATTCATTTA 60
 AAGTAAAATAG CTGCAAAGAC CACATTGGAA AGTCAATGCC AMATGTCCTA GAAGATGAAG 120
 TATATGAAAC AGTTGTAGAT ACCTCTGAAG AAGATAGTTT TTCATTATGT TTTTCTAAAT 180
 GTAGAACAAA AAATCTACAA AAAGTAAGAA CTAGCAAGAC TAGGAAAAAA ATTTTCCATG 240
 AAGCAAACGC TGATGAATGT GAAAAATCTA AAAACCAAGT GAAAGAAAAA TACTCATTTG 300

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1...4987
 - (D) OTHER INFORMATION: Exon 11, nucleotides 20-4951 correspond to nucleotides 2138-7069 of complete coding sequence
- (ix) FEATURE
 - (A) NAME/KEY: variable
 - (B) LOCATION: 339...1917
 - (D) OTHER INFORMATION: Y at positions 339 or 1917 = C or T; R at positions 790, 1081 or 1506 = A or G.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TTTGTGTTTT TATGTTTAGG TTTATTGCAT TCTTCTGTGA AAAGAAGCTG TTCACAGAAT 60
GATTCTGAAG AACCAACTTT GTCCTTAACT AGCTCTTTTG GGACAATTCT GAGGAAATGT 120
TCTAGAAATG AAACATGTTC TAATAATACA GTAATCTCTC AGGATCTTGA TTATAAAGAA 180
GCAAAATGTA ATAAGGAAAA ACTACAGTTA TTTATTACCC CAGAAGCTGA TTCTCTGTCA 240
TGCCTGCAGG AAGGACAGTG TGAAAATGAT CCAAAAAGCA AAAAAGTTTC AGATATAAAA 300
GAAGAGGTCT TGGCTGCAGC ATGTCACCCA GTACAACAYT CAAAAGTGGA ATACAGTGAT 360
ACTGACTTC AATCCCAGAA AAGTCTTTTA TATGATCATG AAAATGCCAG CACTCTTATT 420
TTAACTCCTA CTTCCAAGGA TGTTCTGTCA AACCTAGTCA TGATTTCTAG AGGCAAAGAA 480
TCATACAAAA TGTCAGACAA GCTCAAAGGT AACAATTATG AATCTGATGT TGAATTAACC 540
AAAAATATC CCATGGAAAA GAATCAAGAT GTATGTGCTT TAAATGAAAA TTATAAAAAC 600
GTTGAGCTGT TGCCACCTGA AAAATACATG AGAGTAGCAT CACCTTCAAG AAAGGTACAA 660
TTCAAACAAAA ACACAAATCT AAGAGTAATC CAAAAAAATC CAGGACAATGA GAATAATTTT 720
TCAAAAAATAA CTGTCAATCC AGACCTCTGAA GAACCTTTTCT CAGGACAATGA GAATAATTTT 780

GTCTTCCAAR TAGCTAATGA AAGGAATAAT CTTGCTTTAG GAAATACTAA GGAACTTCAT 840 GAAACAGACT TGACTTGTGT AAACGAACCC ATTTTCAAGA ACTCTACCAT GGTTTTATAT 900 GGAGACACAG GTGATAAACA AGCAACCCAA GTGTCAATTA AAAAAGATTT GGTTTATGTT 960 CTTGCAGAGG AGAACAAAA TAGTGTAAAG CAGCATATAA AAATGACTCT AGGTCAAGAT 1020 TTAAAATCGG ACATCTCCTT GAATATAGAT AAAATACCAG AAAAAAATAA TGATTACATG 1080 RACAAATGGG CAGGACTCTT AGGTCCAATT TCAAATCACA GTTTTGGAGG TAGCTTCAGA 1140 ACAGCTTCAA ATAAGGAAAT CAAGCTCTCT GAACATAACA TTAAGAAGAG CAAAATGTTC 1200 TTCAAAGATA TTGAAGAACA ATATCCTACT AGTTTAGCTT GTGTTGAAAT TGTAAATACC 1260 TTGGCATTAG ATAATCAAAA GAAACTGAGC AAGCCTCAGT CAATTAATAC TGTATCTGCA 1320 CATTTACAGA GTAGTGTAGT TGTTTCTGAT TGTAAAAATA GTCATATAAC CCCTCAGATG 1380 TTATTTTCCA AGCAGGATTT TAATTCAAAC CATAATTTAA CACCTAGCCA AAAGGCAGAA 1440 ATTACAGAAC TTTCTACTAT ATTAGAAGAA TCAGGAAGTC AGTTTGAATT TACTCAGTTT 1500 AGAAARCCAA GCTACATATT GCAGAAGAGT ACATTTGAAG TGCCTGAAAA CCAGATGACT 1560 ATCTTAAAGA CCACTTCTGA GGAATGCAGA GATGCTGATC TTCATGTCAT AATGAATGCC 1620 CCATCGATTG GTCAGGTAGA CAGCAGCAAG CAATTTGAAG GTACAGTTGA AATTAAACGG 1680 AAGTTTGCTG GCCTGTTGAA AAATGACTGT AACAAAAGTG CTTCTGGTTA TTTAACAGAT 1740 GAAAATGAAG TGGGGTTTAG GGGCTTTTAT TCTGCTCATG GCACAAAACT GAATGTTTCT 1800 ACTGAAGCTC TGCAAAAAGC TGTGAAACTG TTTAGTGATA TTGAGAATAT TAGTGAGGAA 1860 ACTTCTGCAG AGGTACATCC AATAAGTTTA TCTTCAAGTA AATGTCATGA TTCTGTYGTT 1920 TCAATGTTTA AGATAGAAAA TCATAATGAT AAAACTGTAA GTGAAAAAAA TAATAAATGC 1980 CAACTGATAT TACAAAATAA TATTGAAATG ACTACTGGCA CTTTTGTTGA AGAAATTACT 2040 GAAAATTACA AGAGAAATAC TGAAAATGAA GATAACAAAT ATACTGCTGC CAGTAGAAAT 2100 TCTCATAACT TAGAATTTGA TGGCAGTGAT TCAAGTAAAA ATGATACTGT TTGTATTCAT 2160 AAAGATGAAA CGGACTTGCT ATTTACTGAT CAGCACAACA TATGTCTTAA ATTATCTGGC 2220 CAGTTTATGA AGGAGGGAAA CACTCAGATT AAAGAAGATT TGTCAGATTT AACTTTTTTT 2280 GAAGTTGCGA AAGCTCAAGA AGCATGTCAT GGTAATACTT CAAATAAAGA ACAGTTAACT 2340 GCTACTAAAA CGGAGCAAAA TATAAAAGAT TTTGAGACTT CTGATACATT TTTTCAGACT 2400 GCAAGTGGGA AAAATATTAG TGTCGCCAAA GAGTCATTTA ATAAAATTGT AAATTTCTTT 2460 GATCAGAAAC CAGAAGAATT GCATAACTTT TCCTTAAATT CTGAATTACA TTCTGACATA 2520 AGAAAGAACA AAATGGACAT TCTAAGTTAT GAGGAAACAG ACATAGTTAA ACACAAAATA 2580 CTGAAAGAAA GTGTCCCAGT TGGTACTGGA AATCAACTAG TGACCTTCCA GGGACAACCC 2640 GAACGTGATG AAAAGATCAA AGAACCTACT CTGTTGGGTT TTCATACAGC TAGCGGGAAA 2700 AAAGTTAAAA TTGCAAAGGA ATCTTTGGAC AAAGTGAAAA ACCTTTTTGA TGAAAAAGAG 2760 CAAGGTACTA GTGAAATCAC CAGTTTTAGC CATCAATGGG CAAAGACCCT AAAGTACAGA 2820 GAGGCCTGTA AAGACCTTGA ATTAGCATGT GAGACCATTG AGATCACAGC TGCCCCAAAG 2880 TGTAAAGAAA TGCAGAATTC TCTCAATAAT GATAAAAACC TTGTTTCTAT TGAGACTGTG 2940 GTGCCACCTA AGCTCTTAAG TGATAATTTA TGTAGACAAA CTGAAAATCT CAAAACATCA 3000 AAAAGTATCT TTTTGAAAGT TAAAGTACAT GAAAATGTAG AAAAAGAAAC AGCAAAAAGT 3060 CCTGCAACTT GTTACACAAA TCAGTCCCCT TATTCAGTCA TTGAAAATTC AGCCTTAGCT 3120 TTTTACACAA GTTGTAGTAG AAAAACTTCT GTGAGTCAGA CTTCATTACT TGAAGCAAAA 3180 AAATGGCTTA GAGAAGGAAT ATTTGATGGT CAACCAGAAA GAATAAATAC TGCAGATTAT 3240 GTAGGAAATT ATTTGTATGA AAATAATTCA AACAGTACTA TAGCTGAAAA TGACAAAAAT 3300 CATCTCTCCG AAAAACAAGA TACTTATTTA AGTAACAGTA GCATGTCTAA CAGCTATTCC 3360 TACCATTCTG ATGAGGTATA TAATGATTCA GGATATCTCT CAAAAAATAA ACTTGATTCT 3420 GGTATTGAGC CAGTATTGAA GAATGTTGAA GATCAAAAAA ACACTAGTTT TTCCAAAGTA 3480 ATATCCAATG TAAAAGATGC AAATGCATAC CCACAAACTG TAAATGAAGA TATTTGCGTT 3540 GAGGAACTTG TGACTAGCTC TTCACCCTGC AAAAATAAAA ATGCAGCCAT TAAATTGTCC 3600 ATATCTAATA GTAATAATTT TGAGGTAGGG CCACCTGCAT TTAGGATAGC CAGTGGTAAA 3660 ATCGTTTGTG TTTCACATGA AACAATTAAA AAAGTGAAAG ACATATTTAC AGACAGTTTC 3720 AGTAAAGTAA TTAAGGAAAA CAACGAGAAT AAATCAAAAA TTTGCCAAAC GAAAATTATG 3780 GCAGGTTGTT ACGAGGCATT GGATGATTCA GAGGATATTC TTCATAACTC TCTAGATAAT 3840 GATGAATGTA GCACGCATTC ACATAAGGTT TTTGCTGACA TTCAGAGTGA AGAAATTTTA 3900

CAACATAACC AAAATATGTC TGGATTGGAG AAAGTTTCTA AAATATCACC TTGTGATGTT 3960 AGTTTGGAAA CTTCAGATAT ATGTAAATGT AGTATAGGGA AGCTTCATAA GTCAGTCTCA 4020 TCTGCAAATA CTTGTGGGAT TTTTAGCACA GCAAGTGGAA AATCTGTCCA GGTATCAGAT 4080 GCTTCATTAC AAAACGCAAG ACAAGTGTTT TCTGAAATAG AAGATAGTAC CAAGCAAGTC 4140 TTTTCCAAAG TATTGTTTAA AAGTAACGAA CATTCAGACC AGCTCACAAG AGAAGAAAAT 4200 ACTGCTATAC GTACTCCAGA ACATTTAATA TCCCAAAAAG GCTTTTCATA TAATGTGGTA 4260 AATTCATCTG CTTTCTCTGG ATTTAGTACA GCAAGTGGAA AGCAAGTTTC CATTTTAGAA 4320 AGTTCCTTAC ACAAAGTTAA GGGAGTGTTA GAGGAATTTG ATTTAATCAG AACTGAGCAT 4380 AGTCTTCACT ATTCACCTAC GTCTAGACAA AATGTATCAA AAATACTTCC TCGTGTTGAT 4440 AAGAGAAACC CAGAGCACTG TGTAAACTCA GAAATGGAAA AAACCTGCAG TAAAGAATTT 4500 AAATTATCAA ATAACTTAAA TGTTGAAGGT GGTTCTTCAG AAAATAATCA CTCTATTAAA 4560 GTTTCTCCAT ATCTCTCA ATTTCAACAA GACAAACAAC AGTTGGTATT AGGAACCAAA 4620 GTCTCACTTG TTGAGAACAT TCATGTTTTG GGAAAAGAAC AGGCTTCACC TAAAAACGTA 4680 AAAATGGAAA TTGGTAAAAC TGAAACTTTT TCTGATGTTC CTGTGAAAAC AAATATAGAA 4740 GTTTGTTCTA CTTACTCCAA AGATTCAGAA AACTACTTTG AAACAGAAGC AGTAGAAATT 4800 GCTAAAGCTT TTATGGAAGA TGATGAACTG ACAGATTCTA AACTGCCAAG TCATGCCACA 4860 CATTCTCTTT TTACATGTCC CGAAAATGAG GAAATGGTTT TGTCAAATTC AAGAATTGGA 4920 AAAAGAAGAG GAGAGCCCCT TATCTTAGTG GGTAAGTGTT CATTTTTACC TTTCGTGTTG 4980 CCAATCA

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1...468
 - (D) OTHER INFORMATION: Exon 14, nucleotides 12-439 correspond to nucleotides 7236-7663 of complete coding sequence
- (ix) FEATURE
 - (A) NAME/KEY: variable
 - (B) LOCATION: 248
 - (D) OTHER INFORMATION: R at position 248 = A or G.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CCCCATTGCA GCACAACTAA GGAACGTCAA GAGATACAGA ATCCAAATTT TACCGCACCT 60
GGTCAAGAAT TTCTGTCTAA ATCTCATTTG TATGAACATC TGACTTTGGA AAAATCTTCA 120
AGCAATTTAG CAGTTTCAGG ACATCCATTT TATCAAGTTT CTGCTACAAG AAATGAAAAA 180
ATGAGACACT TGATTACTAC AGGCAGACCA ACCAAAGTCT TTGTTCCACC TTTTAAAACT 240
AAATCACRTT TTCACAGAGT TGAACAGTGT GTTAGGAATA TTAACTTGGA GGAAAACAGA 300
CAAAAGCAAA ACATTGATGG ACATGGCTCT GATGATAGTA AAAATAAGAT TAATGACAAT 360
GAGATTCATC AGTTTAACAA AAACAACTCC AATCAAGCAG CAGCTGTAAC TTTCACAAAG 420
TGTGAAAGAA AACCTTTAGG TATTGTATGA CAATTTGTGT GATGAATT

(2) INFORMATION FOR SEO ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1...255
 - (D) OTHER INFORMATION: Exon 22, nucleotides 31-229 correspond to nucleotides 8983-9181 of complete coding sequence
- (ix) FEATURE
 - (A) NAME/KEY: variable
 - (B) LOCATION: 127
 - (D) OTHER INFORMATION: R at position 127 = A or G.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTTTTATTCC AATATCTTAA ATGGTCACAG GGTTATTTCA GTGAAGAGCA GTTAAGAGCC 60
TTGAATAATC ACAGGCAAAT GTTGAATGAT AAGAAACAAG CTCAGATCCA GTTGGAAATT 120
AGGAAGRCCA TGGAATCTGC TGAACAAAAG GAACAAGGTT TATCAAGGGA TGTCACAACC 180
GTGTGGAAGT TGCGTATTGT AAGCTATTCA AAAAAAGAAA AAGATTCAGG TAAGTATGTA 240
AATGCTTTGT TTTTA 255

- (2) INFORMATION FOR SEQ ID NO:115:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 31...135
 - (D) OTHER INFORMATION: Exon 2
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TAAGTGCATT TTGGTCTTCT GTTTTGCAGA CTTATTTACC AAGCATTGGA GGAATATCGT 60 AGGTAAAAAT GCCTATTGGA TCCAAAGAGA GGCCAACATT TTTTGAAATT TTTAAGACAC 120 GCTGCAACAA AGCAGGTATT GACAAATTTT ATATAAC 157

- (2) INFORMATION FOR SEQ ID NO:116:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 21...269
 - (D) OTHER INFORMATION: Exon 3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGGATTTTT TTTTAAATAG ATTTAGGACC AATAAGTCTT AATTGGTTTG AAGAACTTTC 60
TTCAGAAGCT CCACCCTATA ATTCTGAACC TGCAGAAGAA TCTGAACATA AAAACAACAA 120
TTACGAACCA AACCTATTTA AAACTCCACA AAGGAAACCA TCTTATAATC AGCTGGCTTC 180
AACTCCAATA ATATTCAAAG AGCAAGGGCT GACTCTGCCG CTGTACCAAT CTCCTGTAAA 240
AGAATTAGAT AAATTCAAAT TAGACTTAGG TAAGTAATGC AATATGGTAG ACTGGGG 297

- (2) INFORMATION FOR SEQ ID NO:117:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 26...134
 - (D) OTHER INFORMATION: Exon 4
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

TCACTGAATT ATTGTACTGT TTCAGGAAGG AATGTTCCCA ATAGTAGACA TAAAAGTCTT 60 CGCACAGTGA AAACTAAAAT GGATCAAGCA GATGATGTT CCTGTCCACT TCTAAATTCT 120 TGTCTTAGTG AAAGGTATGA TGAAGCTATT ATATTAAAA 159

- (2) INFORMATION FOR SEQ ID NO:118:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 31...71
 - (D) OTHER INFORMATION: Exon 6
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTAACAATTT	TCCCCTTTTT	TTACCCCCAG	TGGTATGTGG	GAGTTTGTTT	CATACACCAA	60
AGTTTGTGAA	${\tt GGTAAATATT}$					80

- (2) INFORMATION FOR SEQ ID NO:119:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 51...165
 - (D) OTHER INFORMATION: Exon 7
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TAATGATCAG GGCATTTCTA TAAAAAATAA ACTATTTCT TTCCTCCAG GGTCGTCAGA 60 CACCAAAACA TATTCTGAA AGTCTAGGAG CTGAGGTGGA TCCTGATATG TCTTGGTCAA 120 GTTCTTTAGC TACACCACCC ACCCTTAGTT CTACTGTGCT CATAGGTAAT AATA 174

- (2) INFORMATION FOR SEQ ID NO:120:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 14...63
 - (D) OTHER INFORMATION: Exon 8
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TTTTATCTTA CAGTCAGAAA TGAAGAAGCA TCTGAAACTG TATTTCCTCA TGATACTACT 60 90

- (2) INFORMATION FOR SEQ ID NO:121:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 20...131
- (D) OTHER INFORMATION: Exon 9
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TAAACTATAA TTTTTGCAGA ATGTGAAAAG CTATTTTTCC AATCATGATG AAAGTCTGAA 60 GAAAAATGAT AGATTTATCG CTTCTGTGAC AGACAGTGAA AACACAAATC AAAGAGAAGC 120 TGCAAGTCAT GGTAAGTCCT CT

- (2) INFORMATION FOR SEQ ID NO:122:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 29...124
 - (D) OTHER INFORMATION: Exon 12
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AAAACATATA TGAAATATTT CTTTTTAGGA GAACCCTCAA TCAAAAGAAA CTTATTAAAT 60 GAATTTGACA GGATAATAGA AAATCAAGAA AAATCCTTAA AGGCTTCAAA AAGCACTCCA 120 GATGGTAAAA TTAGCTTTTT ATTTATA

- (2) INFORMATION FOR SEQ ID NO:123:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 31...100
 - (D) OTHER INFORMATION: Exon 13
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

AATATGTAAT ATAAAATAAT TGTTTCCTAG GCACAATAAA AGATCGAAGA TTGTTTATGC 60 ATCATGTTTC TTTAGAGCCG ATTACCTGTG TACCCTTTCG GTAAGACATG TTTAAATTTT 120 TCTAA

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 13...183
 - (D) OTHER INFORMATION: Exon 17
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TTATTTGTTC AGGGCTCTGT GTGACACTCC AGGTGTGGAT CCAAAGCTTA TTTCTAGAAT 60
TTGGGTTTAT AATCACTATA GATGGATCAT ATGGAAACTG GCAGCTATGG AATGTGCCTT 120
TCCTAAGGAA TTTGCTAATA GATGCCTAAG CCCAGAAAGG GTGCTTCTTC AACTAAAATA 180
CAGGCAAGTT TAAAGCATT 1499

- (2) INFORMATION FOR SEQ ID NO:125:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 19...373
 - (D) OTHER INFORMATION: Exon 18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

TTTTGTTTC ACTTTAGAT ATGATACGGA AATTGATAGA AGCAGAAGAT CGGCTATAAA 60

AAAGATAATG GAAAGGGATG ACACAGCTGC AAAAACACTT GTTCTCTGTG TTTCTGACAT 120

AATTTCATTG AGCGCAAATA TATCTGAAAC TTCTAGCAAT AAAACTAGTA GTGCAGATAC 180

CCAAAAAAGTG GCCATTATTG AACTTACAGA TGGGTGGTAT GCTGTTAAGG CCCAGTTAGA 240

TCCTCCCCTC TTAGCTGTCT TAAAGAATGG CAGACTGACA GTTGGTCAGA AGATTATTCT 300

TCATGGAGCA GAACTGGTGG GCTCTCCTGA TGCCTGTACA CCTCTTGAAG CCCCAGAATC 360

TCTTATGTTA AAGGTAAATT

- (2) INFORMATION FOR SEQ ID NO:126:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 30...185
 - (D) OTHER INFORMATION: Exon 19
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

TAAATCAATA TATTTATTAA TTTGTCCAGA TTTCTGCTAA CAGTACTCGG CCTGCTCGCT 60
GGTATACCAA ACTTGGATTC TTTCCTGACC CTAGACCTTT TCCTCTGCCC TTATCATCGC 120
TTTTCAGTGA TGGAGGAAAT GTTGGTTGTG TTGATGTAAT TATTCAAAGA GCATACCCTA 180
TACAGGTATG ATGTATTCTT GAAACTTA 208

- (2) INFORMATION FOR SEQ ID NO:127:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 28...172
 - (D) OTHER INFORMATION: Exon 20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TTTGGTGTGT GTAACACATT ATTACAGTGG ATGGAGAAGA CATCATCTGG ATTATACATA 60
TTTCGCAATG AAAGAGAGA AGAAAAGGAA GCAGCAAAAT ATGTGGAGGC CCAACAAAAG 120
AGACTAGAAG CCTTATTCAC TAAAAATCAG GAGGAATTTG AAGAACATGA AGGTAAAATT 180
AGTTATATGG TACACATTGT TATTTC 206

- (2) INFORMATION FOR SEQ ID NO:128:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 36...157
 - (D) OTHER INFORMATION: Exon 21
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

AGTTTAGTGA ATTAATAATC CTTTTGTTTT CTTAGAAAAC ACAACAAAAC CATATTTACC 60 ATCACGTGCA CTAACAAGAC AGCAAGTTCG TGCTTTGCAA GATGGTGCAG AGCTTTATGA 120 AGCAGTGAAG AATGCAGCAG ACCCAGCTTA CCTTGAGGTG AGAGAGTAAG AGGACATATA 180

- (2) INFORMATION FOR SEQ ID NO:129:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 12...175
 - (D) OTHER INFORMATION: Exon 23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TCTCCAAACA GTTATACTGA GTATTTGGCG TCCATCATCA GATTTATATT CTCTGTTAAC 60
AGAAGGAAG AGATACAGAA TTTATCATCT TGCAACTTCA AAATCTAAAA GTAAATCTGA 120
AAGAGCTAAC ATACAGTTAG CAGCGACAAA AAAAACTCAG TATCAACAAC TACCGGTACA 180
AACCTTTCAT TGTAATTTTT 200

- (2) INFORMATION FOR SEQ ID NO:130:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 25...163
 - (D) OTHER INFORMATION: Exon 24
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATTTTGT TTTGTTTCT GTAGGTTTCA GATGAAATTT TATTCAGAT TTACCAGCCA 60
CGGGAGCCCC TTCACTTCAG CAAATTTTTA GATCCAGACT TTCAGCCATC TTGTTCTGAG 120
GTGGACCTAA TAGGATTTGT CGTTTCTGTT GTGAAAAAAA CAGGTAATGC ACAATATAGT 180
TAATTTTTTT TATTGATTCT TTTAAAAAAAC ATTGTCT 217

- (2) INFORMATION FOR SEQ ID NO:131:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 31...275
 - (D) OTHER INFORMATION: Exon 25
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TAACATTCTT TTCTTTTTT TCCATTCTAG GACTTGCCC TTTCGTCTAT TTGTCAGACG 60
AATGTTACAA TTTACTGGCA ATAAAGTTTT GGATAGACCT TAATGAGGAC ATTATTAAGC 120
CTCATATGTT AATTGCTGCA AGCAACCTCC AGTGGCGACC AGAATCCAAA TCAGGCCTTC 180
TTACTTTATT TGCTGGAGAT TTTTCTGTGT TTTCTGCTAG TCCAAAAGAG GGCCACTTTC 240
AAGAGACATT CAACAAAATG AAAAATACTG TTGAGGTAAG GTTA 284

- (2) INFORMATION FOR SEQ ID NO:132:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 31...177
 - (D) OTHER INFORMATION: Exon 26
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ATAAAGCAGC TTTTCCACTT ATTTCTTAG AATATTGACA TACTTTGCAA TGAAGCAGAA 60 AACAAGCTTA TGCATATACT GCATGCAAAT GATCCCAAGT GGTCCACCC AACTAAAGAC 120 TGTACTTCAG GGCCGTACAC TGCTCAAATC ATTCCTGGTA CAGGAAACAA GCTTCTGGTA 180 AGTTAATGTA AACTCAAGGA ATATTATAAG 210

- (2) INFORMATION FOR SEQ ID NO:133:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 23...691
 - (D) OTHER INFORMATION: Exon 27
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TACGTTTTCA TTTTTTTATC AGATGTCTTC TCCTAATTGT GAGATATATT ATCAAAGTCC 60

TTTATCACTT TGTATGGCCA AAAGGAAGTC TGTTTCCACA CCTGTCTCAG CCCAGATGAC 120
TTCAAAGTCT TGTAAAGGGG AGAAAGAGAT TGATGACCAA AAGAACTGCA AAAAGAAGAAG 180
AGCCTTGGAT TTCTTGAGTA GACTGCCTTT ACCTCCACCT GTTAGTCCCA TTTGTACATT 240
TGTTTCTCCG GCTGCACAGA AGGCATTTCA GCCACCAAGG AGTTGTGGCA CCAAATACGA 300
AACACCCATA AAGAAAAAAG AACTGAATTC TCCTCAGATG ACTCCATTTA AAAAATTCAA 360
TGAAATTTCT CTTTTGGAAA GTAATTCAAT AGCTGACGAA GAACTTGCAT TGATAAATAC 420
CCAAGCTCTT TTGTCTGGTT CAACAGGAGA AAAACAATTT ATATCTGTCA GTGAATCCAC 480
TAGGAACTGCT CCCACCAGTT CAGAAGATTA TCTCAGACTG AAACGACGTT GTACTACATC 540
TCTGATCAAA GAACAGGAGA GTTCCCAGGC CAGTACGGAA GAATGTGAGA AAAATAAGCA 600
GGACACAATT ACAACTAAAA AATATATCTA AGCATTGCA AAGGCGACAA TAAATTATTG 660
ACGCTTAACC TTTCCAGTTT ATAAGACTGG A